

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	306	spondin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L2	249793	antibody or antibodies or immunoglobulin or immunoglobulins	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L3	37	L1 same L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:58
L4	149	mindin	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L5	1	L4 same L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:58
L6	249793	antibody or antibodies or immunoglobulin or immunoglobulins	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L7	1633	RG1 or (RG-1) or (rg adj "1")	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57
L8	28	L7 SAME L6	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/14 10:57

**SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_188\_210.rag.**

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OM protein - protein search, using sw model

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Run on:      May 25, 2006, 11:55:15 ; Search time 18.8418 Seconds
              (without alignments)
              558.119 Million cell updates/sec
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Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPODTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	121	100.0	23	9	ADW76954	Adw76954 Human RG1
2	121	100.0	249	3	AAB34753	Aab34753 Human sec
3	121	100.0	298	8	ADT50840	Adt50840 Cancer re
4	121	100.0	299	3	AAY73490	Aay73490 Human sec
5	121	100.0	330	4	AAE12304	Aae12304 Human NPG
6	121	100.0	330	9	ADW76932	Adw76932 Rat RG1 p
7	121	100.0	331	2	AAW23663	Aaw23663 Human neu
8	121	100.0	331	2	AAW70589	Aaw70589 Adhesion-
9	121	100.0	331	2	AAW83328	Aaw83328 Human min
10	121	100.0	331	2	AAY41721	Aay41721 Human PRO
11	121	100.0	331	2	AAW92460	Aaw92460 Human NAF
12	121	100.0	331	3	AAB33465	Aab33465 Human PRO
13	121	100.0	331	3	AAY79561	Aay79561 Cancer sp
14	121	100.0	331	3	AAB44277	Aab44277 Human PRO
15	121	100.0	331	3	AAY95349	Aay95349 Human PRO
16	121	100.0	331	4	AAM93266	Aam93266 Human pol
17	121	100.0	331	4	AAM93324	Aam93324 Human pol
18	121	100.0	331	4	AAM38872	Aam38872 Human pol
19	121	100.0	331	4	AAB82472	Aab82472 Human ext
20	121	100.0	331	5	ABG61806	Abg61806 Prostate
21	121	100.0	331	5	AAU79944	Aau79944 Human Spo
22	121	100.0	331	5	ABB77393	Abb77393 Human spo
23	121	100.0	331	5	AAE20463	Aae20463 Human tum
24	121	100.0	331	6	ABO25223	Abo25223 Novel hum
25	121	100.0	331	6	ABU72229	Abu72229 Novel hum
26	121	100.0	331	6	ABU84909	Abu84909 Human sec
27	121	100.0	331	6	ABU61107	Abu61107 Human PRO
28	121	100.0	331	6	ABU80376	Abu80376 Human sec
29	121	100.0	331	6	ABG75949	Abg75949 Human ant
30	121	100.0	331	6	ADA24775	Ada24775 Novel hum
31	121	100.0	331	6	ABO19678	Abo19678 Novel hum
32	121	100.0	331	6	ADA12436	Ada12436 Human sec
33	121	100.0	331	6	ABO19569	Abo19569 Novel hum
34	121	100.0	331	7	ADB73742	Adb73742 Human PRO
35	121	100.0	331	7	ADB76458	Adb76458 Human PRO
36	121	100.0	331	7	ADB75561	Adb75561 Prostate
37	121	100.0	331	7	ADC43884	Adc43884 Human sec
38	121	100.0	331	7	ADC61644	Adc61644 Human sec
39	121	100.0	331	7	ADC63608	Adc63608 Human sec
40	121	100.0	331	7	ADC66708	Adc66708 Human sec
41	121	100.0	331	7	ADC68832	Adc68832 Human sec
42	121	100.0	331	7	ADC62892	Adc62892 Human sec
43	121	100.0	331	7	ADC67957	Adc67957 Human sec
44	121	100.0	331	7	ADC41277	Adc41277 Human sec
45	121	100.0	331	7	ADC67332	Adc67332 Human sec

## ALIGNMENTS

## RESULT 1

ADW76954

ID ADW76954 standard; peptide; 23 AA.

XX

AC ADW76954;

XX

DT 07-APR-2005 (first entry)

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279- 2\_copy\_188\_210.ra1.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:07:05 ; Search time 4.80791 Seconds  
(without alignments)  
418.728 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					
No.	Score	Match	Length	ID		Description

1	121	100.0	299	2	US-09-311-021-202	Sequence 202, App
2	121	100.0	330	2	US-09-371-696-2	Sequence 2, Appli
3	121	100.0	330	2	US-09-732-357B-13	Sequence 13, Appl
4	121	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
5	121	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
6	121	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
7	121	100.0	331	2	US-09-949-002-397	Sequence 397, App
8	121	100.0	331	2	US-09-999-833A-236	Sequence 236, App
9	121	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
10	121	100.0	331	2	US-10-020-445A-236	Sequence 236, App
11	121	100.0	331	2	US-09-978-189-236	Sequence 236, App
12	121	100.0	331	2	US-10-017-085A-236	Sequence 236, App
13	121	100.0	331	3	US-10-145-129A-236	Sequence 236, App
14	121	100.0	331	3	US-10-013-929A-236	Sequence 236, App
15	121	100.0	331	3	US-10-013-917A-236	Sequence 236, App
16	121	100.0	422	2	US-09-949-002-504	Sequence 504, App
17	116	95.9	23	2	US-09-732-357B-11	Sequence 11, Appl
18	86	71.1	568	1	US-07-862-021B-14	Sequence 14, Appl
19	86	71.1	568	5	PCT-US93-03164-14	Sequence 14, Appl
20	82	67.8	392	1	US-08-799-173A-7	Sequence 7, Appli
21	82	67.8	392	2	US-09-170-042A-7	Sequence 7, Appli
22	82	67.8	787	2	US-09-825-294-207	Sequence 207, App
23	82	67.8	787	2	US-09-970-966-207	Sequence 207, App
24	82	67.8	807	1	US-07-862-021B-10	Sequence 10, Appl
25	82	67.8	807	1	US-08-313-288B-10	Sequence 10, Appl
26	82	67.8	807	2	US-09-132-769-1	Sequence 1, Appli
27	82	67.8	807	2	US-09-132-769-3	Sequence 3, Appli
28	82	67.8	807	2	US-09-132-769-5	Sequence 5, Appli
29	82	67.8	807	2	US-09-640-173-186	Sequence 186, App
30	82	67.8	807	2	US-09-713-550-186	Sequence 186, App
31	82	67.8	807	2	US-09-825-294-186	Sequence 186, App
32	82	67.8	807	2	US-09-970-966-186	Sequence 186, App
33	82	67.8	807	5	PCT-US93-03164-10	Sequence 10, Appl
34	81	66.9	802	1	US-07-862-021B-12	Sequence 12, Appl
35	81	66.9	802	1	US-08-313-288B-12	Sequence 12, Appl
36	81	66.9	802	5	PCT-US93-03164-12	Sequence 12, Appl
37	61	50.4	23	2	US-09-132-769-19	Sequence 19, Appl
38	55	45.5	677	2	US-09-270-767-58094	Sequence 58094, A
39	55	45.5	847	2	US-09-270-767-42783	Sequence 42783, A
40	54	44.6	819	2	US-09-270-767-42963	Sequence 42963, A
41	48.5	40.1	838	3	US-10-420-191-2	Sequence 2, Appli
42	47	38.8	424	2	US-09-328-352-4377	Sequence 4377, Ap
43	46	38.0	863	2	US-09-619-353-14	Sequence 14, Appl
44	46	38.0	1198	2	US-09-199-637A-405	Sequence 405, App
45	45.5	37.6	489	2	US-09-771-161A-176	Sequence 176, App

## ALIGNMENTS

## RESULT 1

US-09-311-021-202

; Sequence 202, Application US/09311021

; Patent No. 6706869

; GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Agostino, Michael J.

; APPLICANT: Genetics Institute, Inc.

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_188\_210.rapbm.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:39 ; Search time 16.048 Seconds  
(without alignments)  
663.879 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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1	121	100.0	330	3	US-09-903-383-2	Sequence 2, Appli
2	121	100.0	330	3	US-09-970-944-41	Sequence 41, Appl
3	121	100.0	330	4	US-10-616-279-13	Sequence 13, Appl
4	121	100.0	330	4	US-10-624-884-13	Sequence 13, Appl
5	121	100.0	330	5	US-10-895-183-13	Sequence 13, Appl
6	121	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
7	121	100.0	331	3	US-09-978-295A-236	Sequence 236, App
8	121	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
9	121	100.0	331	3	US-09-978-697-236	Sequence 236, App
10	121	100.0	331	3	US-09-978-192A-236	Sequence 236, App
11	121	100.0	331	3	US-09-999-832A-236	Sequence 236, App
12	121	100.0	331	3	US-09-978-189-236	Sequence 236, App
13	121	100.0	331	3	US-09-978-608A-236	Sequence 236, App
14	121	100.0	331	3	US-09-978-585A-236	Sequence 236, App
15	121	100.0	331	3	US-09-978-191A-236	Sequence 236, App
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17	121	100.0	331	3	US-09-978-564A-236	Sequence 236, App
18	121	100.0	331	3	US-09-999-833A-236	Sequence 236, App
19	121	100.0	331	3	US-09-981-915A-236	Sequence 236, App
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27	121	100.0	331	3	US-09-978-187B-236	Sequence 236, App
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35	121	100.0	331	3	US-09-978-299A-236	Sequence 236, App
36	121	100.0	331	3	US-09-978-544A-236	Sequence 236, App
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38	121	100.0	331	3	US-09-978-802A-236	Sequence 236, App
39	121	100.0	331	3	US-09-970-944-12	Sequence 12, Appl
40	121	100.0	331	3	US-09-970-944-38	Sequence 38, Appl
41	121	100.0	331	3	US-09-970-944-39	Sequence 39, Appl
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43	121	100.0	331	3	US-09-999-831A-236	Sequence 236, App
44	121	100.0	331	3	US-09-978-824-236	Sequence 236, App
45	121	100.0	331	4	US-10-017-081A-236	Sequence 236, App

## ALIGNMENTS

## RESULT 1

US-09-903-383-2

; Sequence 2, Application US/09903383

; Patent No. US20020137135A1

; GENERAL INFORMATION:

; APPLICANT: Sytkowski, Arthur J.

; APPLICANT: Yang, Meiheng

; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE

; TITLE OF INVENTION: TUMORS

; FILE REFERENCE: 01948/053002

; CURRENT APPLICATION NUMBER: US/09/903,383

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:59 ; Search time 1.03955 Seconds  
(without alignments)  
246.414 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result                      %  
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No.	Score	Match	Length	DB	ID	Description
1	44	36.4	258	6	US-10-953-349-18735	Sequence 18735, A
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3	44	36.4	268	6	US-10-953-349-18733	Sequence 18733, A
4	44	36.4	315	6	US-10-953-349-20835	Sequence 20835, A
5	44	36.4	334	6	US-10-953-349-20834	Sequence 20834, A
6	44	36.4	344	6	US-10-953-349-20833	Sequence 20833, A
7	44	36.4	448	7	US-11-293-697-3667	Sequence 3667, Ap
8	42	34.7	1338	6	US-10-505-928-634	Sequence 634, App
9	42	34.7	1338	6	US-10-505-928-857	Sequence 857, App
10	41	33.9	381	6	US-10-953-349-21878	Sequence 21878, A
11	40	33.1	208	6	US-10-953-349-16383	Sequence 16383, A
12	40	33.1	280	6	US-10-953-349-16382	Sequence 16382, A
13	40	33.1	342	6	US-10-953-349-16381	Sequence 16381, A
14	40	33.1	408	6	US-10-953-349-32202	Sequence 32202, A
15	40	33.1	425	6	US-10-953-349-32201	Sequence 32201, A
16	40	33.1	462	6	US-10-953-349-32200	Sequence 32200, A
17	40	33.1	881	7	US-11-121-154-170	Sequence 170, App
18	39.5	32.6	117	6	US-10-968-757-3	Sequence 3, Appli
19	39.5	32.6	117	6	US-10-968-757-11	Sequence 11, Appl
20	39.5	32.6	279	6	US-10-968-757-2	Sequence 2, Appli
21	39	32.2	286	6	US-10-953-349-6607	Sequence 6607, Ap
22	39	32.2	367	7	US-11-253-300-29	Sequence 29, Appl
23	39	32.2	413	6	US-10-953-349-846	Sequence 846, App
24	39	32.2	431	6	US-10-953-349-845	Sequence 845, App
25	38.5	31.8	101	6	US-10-953-349-27180	Sequence 27180, A
26	38.5	31.8	167	6	US-10-953-349-27179	Sequence 27179, A
27	38.5	31.8	181	6	US-10-953-349-27178	Sequence 27178, A
28	38	31.4	329	6	US-10-953-349-21779	Sequence 21779, A
29	38	31.4	334	6	US-10-953-349-21778	Sequence 21778, A
30	38	31.4	367	6	US-10-953-349-21777	Sequence 21777, A
31	38	31.4	666	6	US-10-953-349-3549	Sequence 3549, Ap
32	38	31.4	690	6	US-10-953-349-3548	Sequence 3548, Ap
33	38	31.4	902	6	US-10-953-349-3547	Sequence 3547, Ap
34	38	31.4	1189	7	US-11-311-778-20	Sequence 20, Appl
35	37.5	31.0	290	6	US-10-953-349-3888	Sequence 3888, Ap
36	37.5	31.0	307	6	US-10-953-349-10430	Sequence 10430, A
37	37.5	31.0	351	6	US-10-953-349-10429	Sequence 10429, A
38	37.5	31.0	388	6	US-10-953-349-10428	Sequence 10428, A
39	37.5	31.0	412	6	US-10-953-349-22821	Sequence 22821, A
40	37.5	31.0	442	6	US-10-953-349-22820	Sequence 22820, A
41	37.5	31.0	463	6	US-10-953-349-3887	Sequence 3887, Ap
42	37.5	31.0	469	6	US-10-953-349-3886	Sequence 3886, Ap
43	37	30.6	119	7	US-11-300-563-11	Sequence 11, Appl
44	37	30.6	217	6	US-10-953-349-5801	Sequence 5801, Ap
45	37	30.6	219	6	US-10-953-349-5800	Sequence 5800, Ap

## ALIGNMENTS

## RESULT 1

US-10-953-349-18735

; Sequence 18735, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

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A;Cross-references: UNIPROT:O53444; UNIPARC:UPI00000D5EAA; GB:AL021897; GB:AL123456; AB0221 probable sugar-binding periplasmic protein YPO1813 [imported] - Yersinia pestis (strain CC N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Ruth PID:g15979836; GSPDB:GN00175 C;Genetics: A;Gene: YPO1813 Query Match 38.0%; Score 46; I T10666 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 393/3; thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence\_revis source: cultivar Columbia; BAC clone F8D20 C;Genetics: A;Map position: 4 A;Introns: 13/3; 58/2; cytochrome c2, iso-2 - Rhodospirillum molischianum C;Species: Rhodospirillum molischianum C;Da protein A;Residues: 1-97 A;Cross-references: UNIPROT:P00088; UNIPARC:UPI0000128854 C;Supr Conservative 1; Mismatches 3; Indels 0; Gaps 0; Qy 2 AGTDSGFTFSSPN 14 ||| ||| || |: Db 35 AGT ferredoxin from the nonheterocystous, nitrogen-fixing cyanobacterium Plectonema boryanum PCC 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 5 DSGFTFSSPN 14 |||| ||:|| Db 88 DSGFKI

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:00:39 ; Search time 3.11864 Seconds  
(without alignments)  
709.599 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0.  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	71.1	803	2	A47723	F-spondin precursor
2	82	67.8	807	2	A38152	F-spondin - rat
3	67	55.4	805	2	T34212	hypothetical prote
4	50	41.3	678	2	G65104	hypothetical 72.8
5	50	41.3	678	2	D91132	probable glycosyla
6	50	41.3	678	2	G85977	probable glycosyla
7	48	39.7	118	2	S04873	hypothetical prote
8	47	38.8	135	2	T09238	hypothetical prote
9	47	38.8	237	2	E84211	hypothetical prote
10	46.5	38.4	291	2	F70896	hypothetical prote
11	46	38.0	331	2	AB0221	probable sugar-bin
12	46	38.0	670	2	T10666	hypothetical prote
13	46	38.0	917	2	T04661	hypothetical prote
14	45	37.2	97	1	CCQFM2	cytochrome c2, iso
15	45	37.2	121	2	B49890	fdxH 5'-region hyp
16	45	37.2	291	2	T49260	hypothetical prote
17	45	37.2	312	2	T08282	regulatory protein
18	45	37.2	412	2	C84518	hypothetical prote
19	45	37.2	426	2	C97797	tetrahydrofolylpol
20	45	37.2	901	2	T03726	capsid polyprotein
21	45	37.2	3224	1	S58884	Ran-binding protei
22	44	36.4	103	2	A55223	hypothetical prote
23	44	36.4	117	1	MHDGMO	Ig heavy chain V r
24	44	36.4	433	2	G71657	folylpolyglutamate
25	44	36.4	492	2	A97429	flgK protein prote
26	44	36.4	492	2	AB2647	hook associated pr
27	44	36.4	702	2	T13058	NADH2 dehydrogenas
28	44	36.4	1034	2	T30331	P-glycoprotein - T
29	44	36.4	1265	2	S57968	Ran-binding protei
30	43.5	36.0	1147	2	S64930	serine/threonine-s
31	43	35.5	117	2	H71180	hypothetical prote
32	43	35.5	221	2	AH2510	hypothetical prote
33	43	35.5	372	2	T42535	leucine-tRNA ligas
34	43	35.5	379	2	AI2267	hypothetical prote
35	43	35.5	394	2	G84206	hypothetical prote
36	43	35.5	449	2	G64597	UDP-N-acetylmurama
37	43	35.5	472	2	B56954	yes-associated pro
38	43	35.5	513	2	T38044	hypothetical prote
39	43	35.5	600	2	T38798	hypothetical prote
40	43	35.5	990	2	A86215	protein T6D22.8 [i
41	43	35.5	1038	2	AG2187	hypothetical prote
42	43	35.5	1111	2	T38407	leucyl-trna synthe
43	43	35.5	1819	2	D97033	uncharacterized pr
44	43	35.5	2090	2	S26058	probable transform
45	42.5	35.1	213	2	A84250	NADH oxidase [impo

## ALIGNMENTS

## RESULT 1

A47723

F-spondin precursor - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_188\_210.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:55:28 ; Search time 24.9492 Seconds  
(without alignments)  
852.749 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_188\_210  
Perfect score: 121  
Sequence: 1 DAGTDSGFTFSSPNFATIPQDTV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	121	100.0	216	2	Q9H7I1_HUMAN	Q9h7i1 homo sapien
2	121	100.0	289	2	Q6KAS6_MOUSE	Q6kas6 mus musculu
3	121	100.0	330	1	SPON2_MOUSE	Q8bms2 mus musculu
4	121	100.0	330	1	SPON2_RAT	Q9wv75 rattus norv

5	121	100.0	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
6	121	100.0	331	1	SPON2_HUMAN	Q9bud6	homo sapien
7	121	100.0	331	2	Q4W5N4_HUMAN	Q4w5n4	homo sapien
8	121	100.0	331	2	Q5RFG6_PONPY	Q5rfg6	pongo pygma
9	114	94.2	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
10	110	90.9	331	2	O42112_BRARE	O42112	brachydanio
11	109	90.1	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon n
12	95	78.5	334	2	O42111_BRARE	O42111	brachydanio
13	93	76.9	280	2	Q4SDS0_TETNG	Q4sds0	tetraodon n
14	86	71.1	803	1	SPON1_XENLA	P35447	xenopus lae
15	84	69.4	598	2	O02029_DROME	O02029	drosophila
16	82	67.8	557	2	Q4SPB7_TETNG	Q4spb7	tetraodon n
17	82	67.8	601	2	Q9V746_DROME	Q9v746	drosophila
18	82	67.8	729	2	Q69ZZ7_MOUSE	Q69zz7	mus musculu
19	82	67.8	807	1	SPON1_BOVIN	Q9glx9	bos taurus
20	82	67.8	807	1	SPON1_HUMAN	Q9hcb6	homo sapien
21	82	67.8	807	1	SPON1_MOUSE	Q8vcc9	mus musculu
22	82	67.8	807	1	SPON1_RAT	P35446	rattus norv
23	82	67.8	807	2	Q3B7D6_RAT	Q3b7d6	rattus norv
24	81	66.9	802	1	SPON1_CHICK	Q9w770	gallus gall
25	80	66.1	806	2	Q4SOW9_TETNG	Q4sow9	tetraodon n
26	75	62.0	808	2	O42113_BRARE	O42113	brachydanio
27	74	61.2	803	2	O42114_BRARE	O42114	brachydanio
28	72	59.5	898	2	O76822_BRAFL	O76822	branchiosto
29	67	55.4	819	2	Q19305_CAEEL	Q19305	caenorhabdi
30	67	55.4	820	2	Q61C53_CAEER	Q61c53	caenorhabdi
31	64	52.9	461	2	Q95S22_DROME	Q95s22	drosophila
32	64	52.9	628	2	Q7KRF4_DROME	Q7krf4	drosophila
33	64	52.9	763	2	Q9XZD0_DROME	Q9xzd0	drosophila
34	60	49.6	505	2	Q5TN62_ANOGA	Q5tn62	anopheles g
35	60	49.6	845	2	Q7Q082_ANOGA	Q7q082	anopheles g
36	58	47.9	632	2	Q5TMM3_ANOGA	Q5tmm3	anopheles g
37	58	47.9	781	2	Q7PZ75_ANOGA	Q7pz75	anopheles g
38	55	45.5	549	2	Q8T988_DROME	Q8t988	drosophila
39	55	45.5	839	2	Q8ML26_DROME	Q8ml26	drosophila
40	54	44.6	873	2	Q7KR42_DROME	Q7kr42	drosophila
41	52	43.0	110	2	Q2RS24_RHORU	Q2rs24	rhodospiril
42	52	43.0	661	2	Q7U449_SYNPX	Q7u449	synechococc
43	52	43.0	1521	2	Q8CHS9_MOUSE	Q8chs9	mus musculu
44	52	43.0	2112	2	Q80U93_MOUSE	Q80u93	mus musculu
45	51	42.1	184	2	Q4FXG8_LEIMA	Q4fxg8	leishmania

## ALIGNMENTS

## RESULT 1

Q9H7I1\_HUMAN

ID Q9H7I1\_HUMAN PRELIMINARY; PRT; 216 AA.

AC Q9H7I1;

DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2001, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE FLJ00108 protein (Fragment).

GN Name=FLJ00108;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

## SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279- 2\_copy\_263\_274.rag.

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<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:19 ; Search time 96.2609 Seconds  
(without alignments)  
56.997 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_263\_274  
Perfect score: 58  
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	12	4	AAB82476	Aab82476 Human ext
2	58	100.0	12	9	ADW76931	Adw76931 Human RG1
3	58	100.0	249	3	AAB34753	Aab34753 Human sec
4	58	100.0	299	3	AAY73490	Aay73490 Human sec
5	58	100.0	331	2	AAW23663	Aaw23663 Human neu
6	58	100.0	331	2	AAW70589	Aaw70589 Adhesion-
7	58	100.0	331	2	AAW83328	Aaw83328 Human min
8	58	100.0	331	2	AAY41721	Aay41721 Human PRO
9	58	100.0	331	2	AAW92460	Aaw92460 Human NAF
10	58	100.0	331	3	AAB33465	Aab33465 Human PRO
11	58	100.0	331	3	AAY79561	Aay79561 Cancer sp
12	58	100.0	331	3	AAB44277	Aab44277 Human PRO
13	58	100.0	331	3	AAY95349	Aay95349 Human PRO
14	58	100.0	331	4	AAM93266	Aam93266 Human pol
15	58	100.0	331	4	AAM93324	Aam93324 Human pol
16	58	100.0	331	4	AAM38872	Aam38872 Human pol
17	58	100.0	331	4	AAB82472	Aab82472 Human ext
18	58	100.0	331	5	ABG61806	Abg61806 Prostate
19	58	100.0	331	5	AAU79944	Aau79944 Human Spo
20	58	100.0	331	5	ABB77393	Abb77393 Human spo
21	58	100.0	331	5	AAE20463	Aae20463 Human tum
22	58	100.0	331	6	ABO25223	Abo25223 Novel hum
23	58	100.0	331	6	ABU72229	Abu72229 Novel hum
24	58	100.0	331	6	ABU84909	Abu84909 Human sec
25	58	100.0	331	6	ABU61107	Abu61107 Human PRO
26	58	100.0	331	6	ABU80376	Abu80376 Human sec
27	58	100.0	331	6	ABG75949	Abg75949 Human ant
28	58	100.0	331	6	ADA24775	Ada24775 Novel hum
29	58	100.0	331	6	ABO19678	Abo19678 Novel hum
30	58	100.0	331	6	ADA12436	Ada12436 Human sec
31	58	100.0	331	6	ABO19569	Abo19569 Novel hum
32	58	100.0	331	7	ADB73742	Adb73742 Human PRO
33	58	100.0	331	7	ADB76458	Adb76458 Human PRO
34	58	100.0	331	7	ADB75561	Adb75561 Prostate
35	58	100.0	331	7	ADC43884	Adc43884 Human sec
36	58	100.0	331	7	ADC61644	Adc61644 Human sec
37	58	100.0	331	7	ADC63608	Adc63608 Human sec
38	58	100.0	331	7	ADC66708	Adc66708 Human sec
39	58	100.0	331	7	ADC68832	Adc68832 Human sec
40	58	100.0	331	7	ADC62892	Adc62892 Human sec
41	58	100.0	331	7	ADC67957	Adc67957 Human sec
42	58	100.0	331	7	ADC41277	Adc41277 Human sec
43	58	100.0	331	7	ADC67332	Adc67332 Human sec
44	58	100.0	331	7	ADC62268	Adc62268 Human sec
45	58	100.0	331	7	ADC41901	Adc41901 Human sec
46	58	100.0	331	7	ADE49270	Ade49270 Human sec
47	58	100.0	331	7	ADE35324	Ade35324 Human sec
48	58	100.0	331	7	ADE16438	Adel6438 Human sec
49	58	100.0	331	7	ADD73053	Add73053 Human sec
50	58	100.0	331	7	ADD72411	Add72411 Human sec
51	58	100.0	331	7	ADE17062	Adel17062 Human sec
52	58	100.0	331	7	ADF47076	Adf47076 Human sec
53	58	100.0	331	7	ADG42579	Adg42579 Novel hum
54	58	100.0	331	7	ADG42585	Adg42585 Human ext
55	58	100.0	331	7	ADG42586	Adg42586 Human ext
56	58	100.0	331	7	ADG42587	Adg42587 Human ext
57	58	100.0	331	7	ADG52833	Adg52833 Human sec

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_263\_274.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 24.7826 Seconds  
(without alignments)  
42.383 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_263\_274  
Perfect score: 58  
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
-----		



1	58	100.0	12	2	US-09-732-357B-12	Sequence 12, Appl
2	58	100.0	299	2	US-09-311-021-202	Sequence 202, App
3	58	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
4	58	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
5	58	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
6	58	100.0	331	2	US-09-949-002-397	Sequence 397, App
7	58	100.0	331	2	US-09-999-833A-236	Sequence 236, App
8	58	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
9	58	100.0	331	2	US-10-020-445A-236	Sequence 236, App
10	58	100.0	331	2	US-09-978-189-236	Sequence 236, App
11	58	100.0	331	2	US-10-017-085A-236	Sequence 236, App
12	58	100.0	331	3	US-10-145-129A-236	Sequence 236, App
13	58	100.0	331	3	US-10-013-929A-236	Sequence 236, App
14	58	100.0	331	3	US-10-013-917A-236	Sequence 236, App
15	58	100.0	422	2	US-09-949-002-504	Sequence 504, App
16	53	91.4	330	2	US-09-732-357B-13	Sequence 13, Appl
17	50	86.2	37	2	US-09-022-238-3	Sequence 3, Appli
18	50	86.2	37	2	US-09-371-696-3	Sequence 3, Appli
19	50	86.2	132	2	US-09-022-238-2	Sequence 2, Appli
20	50	86.2	330	2	US-09-371-696-2	Sequence 2, Appli
21	37	63.8	717	1	US-08-435-925C-2	Sequence 2, Appli
22	37	63.8	749	2	US-09-562-737-96	Sequence 96, Appl
23	36	62.1	141	2	US-09-270-767-45511	Sequence 45511, A
24	36	62.1	190	2	US-09-605-703B-2504	Sequence 2504, Ap
25	36	62.1	256	2	US-09-305-489-2	Sequence 2, Appli
26	36	62.1	408	2	US-09-252-991A-33131	Sequence 33131, A
27	36	62.1	2216	2	US-09-902-540-12221	Sequence 12221, A
28	35	60.3	70	2	US-09-252-991A-26553	Sequence 26553, A
29	35	60.3	297	2	US-09-252-991A-28307	Sequence 28307, A
30	35	60.3	578	2	US-09-949-016-6715	Sequence 6715, Ap
31	35	60.3	583	2	US-09-949-016-9840	Sequence 9840, Ap
32	35	60.3	904	2	US-09-543-681A-6943	Sequence 6943, Ap
33	34	58.6	127	2	US-09-270-767-42359	Sequence 42359, A
34	34	58.6	161	2	US-09-107-532A-6131	Sequence 6131, Ap
35	34	58.6	178	2	US-09-540-236-2174	Sequence 2174, Ap
36	34	58.6	188	2	US-09-252-991A-18537	Sequence 18537, A
37	34	58.6	241	2	US-09-825-414-22	Sequence 22, Appl
38	34	58.6	360	2	US-09-252-991A-26691	Sequence 26691, A
39	34	58.6	474	2	US-09-732-615-12	Sequence 12, Appl
40	34	58.6	474	2	US-10-273-051-12	Sequence 12, Appl
41	34	58.6	826	2	US-09-830-762-5	Sequence 5, Appli
42	34	58.6	854	2	US-09-830-762-2	Sequence 2, Appli
43	33	56.9	154	2	US-09-270-767-57940	Sequence 57940, A
44	33	56.9	189	2	US-09-605-703B-1300	Sequence 1300, Ap
45	33	56.9	195	2	US-09-248-796A-27805	Sequence 27805, A
46	33	56.9	205	2	US-09-252-991A-24792	Sequence 24792, A
47	33	56.9	232	1	US-08-956-047-36	Sequence 36, Appl
48	33	56.9	252	5	PCT-US96-01314-56	Sequence 56, Appl
49	33	56.9	271	5	PCT-US95-02455-2	Sequence 2, Appli
50	33	56.9	273	2	US-09-248-796A-15037	Sequence 15037, A
51	33	56.9	312	2	US-09-475-316A-64	Sequence 64, Appl
52	33	56.9	312	2	US-09-704-640-64	Sequence 64, Appl
53	33	56.9	429	1	US-08-745-977-4	Sequence 4, Appli
54	33	56.9	429	2	US-09-040-699A-4	Sequence 4, Appli
55	33	56.9	532	2	US-09-270-767-46369	Sequence 46369, A
56	33	56.9	643	2	US-09-178-252-25	Sequence 25, Appl
57	33	56.9	643	2	US-09-826-660-25	Sequence 25, Appl
58	33	56.9	653	2	US-09-661-322A-6	Sequence 6, Appli
59	33	56.9	799	2	US-10-094-749-1917	Sequence 1917, Ap
60	33	56.9	1186	2	US-09-178-252-23	Sequence 23, Appl
61	33	56.9	1186	2	US-09-826-660-23	Sequence 23, Appl

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_263\_274.rapbn.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 5.21739 Seconds  
(without alignments)  
25.616 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_263\_274  
Perfect score: 58  
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result    %  
Query

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1	36	62.1	19	7	US-11-122-986-686	Sequence 686, App
2	36	62.1	464	7	US-11-122-986-239	Sequence 239, App
3	36	62.1	464	7	US-11-122-986-241	Sequence 241, App
4	33	56.9	192	6	US-10-953-349-36740	Sequence 36740, A
5	33	56.9	205	6	US-10-953-349-36739	Sequence 36739, A
6	33	56.9	257	6	US-10-953-349-36738	Sequence 36738, A
7	33	56.9	304	6	US-10-953-349-6569	Sequence 6569, Ap
8	33	56.9	324	6	US-10-953-349-11519	Sequence 11519, A
9	33	56.9	340	6	US-10-953-349-28435	Sequence 28435, A
10	33	56.9	360	6	US-10-953-349-6568	Sequence 6568, Ap
11	33	56.9	366	6	US-10-953-349-28434	Sequence 28434, A
12	33	56.9	397	6	US-10-953-349-6567	Sequence 6567, Ap
13	33	56.9	1822	6	US-10-505-928-700	Sequence 700, App
14	32	55.2	361	6	US-10-953-349-707	Sequence 707, App
15	32	55.2	373	6	US-10-953-349-706	Sequence 706, App
16	32	55.2	396	6	US-10-953-349-4090	Sequence 4090, Ap
17	32	55.2	421	6	US-10-953-349-4089	Sequence 4089, Ap
18	32	55.2	580	6	US-10-953-349-12416	Sequence 12416, A
19	32	55.2	619	6	US-10-953-349-12415	Sequence 12415, A
20	32	55.2	621	6	US-10-953-349-12414	Sequence 12414, A
21	31	53.4	198	6	US-10-953-349-26364	Sequence 26364, A
22	31	53.4	222	7	US-11-293-697-4522	Sequence 4522, Ap
23	31	53.4	242	6	US-10-953-349-26363	Sequence 26363, A
24	31	53.4	253	7	US-11-293-697-4349	Sequence 4349, Ap
25	31	53.4	255	6	US-10-953-349-38691	Sequence 38691, A
26	31	53.4	310	6	US-10-953-349-38690	Sequence 38690, A
27	31	53.4	325	6	US-10-953-349-38689	Sequence 38689, A
28	31	53.4	495	6	US-10-953-349-22310	Sequence 22310, A
29	31	53.4	580	6	US-10-953-349-1290	Sequence 1290, Ap
30	31	53.4	737	6	US-10-953-349-1289	Sequence 1289, Ap
31	31	53.4	870	6	US-10-953-349-1288	Sequence 1288, Ap
32	30	51.7	68	6	US-10-953-349-27055	Sequence 27055, A
33	30	51.7	95	6	US-10-953-349-18359	Sequence 18359, A
34	30	51.7	105	6	US-10-953-349-4253	Sequence 4253, Ap
35	30	51.7	105	6	US-10-953-349-6846	Sequence 6846, Ap
36	30	51.7	120	7	US-11-293-697-4269	Sequence 4269, Ap
37	30	51.7	135	6	US-10-953-349-4252	Sequence 4252, Ap
38	30	51.7	135	6	US-10-953-349-6845	Sequence 6845, Ap
39	30	51.7	142	6	US-10-953-349-18358	Sequence 18358, A
40	30	51.7	171	6	US-10-953-349-18357	Sequence 18357, A
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42	30	51.7	186	6	US-10-953-349-6844	Sequence 6844, Ap
43	30	51.7	221	6	US-10-953-349-17730	Sequence 17730, A
44	30	51.7	275	6	US-10-953-349-24566	Sequence 24566, A
45	30	51.7	277	6	US-10-953-349-17729	Sequence 17729, A
46	30	51.7	279	6	US-10-953-349-19383	Sequence 19383, A
47	30	51.7	317	6	US-10-953-349-24565	Sequence 24565, A
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49	30	51.7	354	6	US-10-953-349-23264	Sequence 23264, A
50	30	51.7	401	6	US-10-953-349-24564	Sequence 24564, A
51	30	51.7	415	6	US-10-953-349-4574	Sequence 4574, Ap
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53	30	51.7	511	7	US-11-121-154-96	Sequence 96, Appl
54	30	51.7	515	6	US-10-953-349-6305	Sequence 6305, Ap
55	30	51.7	517	6	US-10-953-349-4573	Sequence 4573, Ap
56	30	51.7	540	6	US-10-953-349-6304	Sequence 6304, Ap
57	30	51.7	553	6	US-10-953-349-4572	Sequence 4572, Ap
58	29	50.0	64	6	US-10-953-349-9704	Sequence 9704, Ap
59	29	50.0	71	6	US-10-953-349-38080	Sequence 38080, A

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 86.6087 Seconds  
(without alignments)  
64.180 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_263\_274  
Perfect score: 58  
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*

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- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	58	100.0	12	3	US-09-732-357A-12	Sequence 12, Appl
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4	58	100.0	12	5	US-10-895-183-12	Sequence 12, Appl
5	58	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
6	58	100.0	331	3	US-09-978-295A-236	Sequence 236, App
7	58	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
8	58	100.0	331	3	US-09-978-697-236	Sequence 236, App
9	58	100.0	331	3	US-09-978-192A-236	Sequence 236, App
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14	58	100.0	331	3	US-09-978-191A-236	Sequence 236, App
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17	58	100.0	331	3	US-09-999-833A-236	Sequence 236, App
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19	58	100.0	331	3	US-09-978-824-236	Sequence 236, App
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23	58	100.0	331	3	US-09-978-193A-236	Sequence 236, App
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41	58	100.0	331	3	US-09-970-944-40	Sequence 40, Appl
42	58	100.0	331	3	US-09-999-831A-236	Sequence 236, App
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http://es/ScoreAccessWeb/GetItem.action?AppId=10616279&seqId=523224&ItemName=us... 6/14/06

Mismatches 1; Indels 0; Gaps 0; Qy 3 IVDSASVPE 11 |||:| ||| Db 158 IVDAAEVPE 166 RESULT 22 and legumes. A;Reference number: Z14734; MUID:97305956; PMID:9163424 A;Accession: T4706 VDSASVPET 12 || |:|:| Db 83 VDGASIPQT 91 RESULT 23 S04718 DNA-directed RNA polymerase (RNA polymerase of the archaebacterium *Sulfolobus acidocaldarius*. A;Reference number: S04714; F.; Garrett, R.A.; Zillig, W. Proc. Natl. Acad. Sci. U.S.A. 86, 4569-4573, 1989 A;Title: Archaebacter C;Genetics: A;Gene: rpoC C;Function: A;Description: (EC 2.7.7.6) [validated, MUID:89315197] C; *Sulfolobus solfataricus* C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15- Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank DB 2; Length 395; Best Local Similarity 63.6%; Pred. No. 71; Matches 7; Conservative 1; Mismatch M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Brooks, K.; C number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0350 A;Status: preliminary A Conservative 3; Mismatches 2; Indels 0; Gaps 0; Qy 2 EIVDSASVPET 12 |:| ||:| | Db 242 ELLDKA K. Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic b source: strain C-125 C;Genetics: A;Gene: dacA C;Superfamily: penicillin-binding protein 5 Query M #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004 C;Accession: S54025; S28567 R;Lye Library, November 1992 A;Description: MSS1 a nuclear-encoded mitochondrial GTPase involved in 13R A;Genome: nuclear C;Superfamily: thiophen / furan oxidation protein; translation elongation f NEIVDSASVP 10 | :|||:| Db 67 NRLVDSSTVP 76 RESULT 28 F86648 hypothetical protein ybjJ [im bacterium *Lactococcus lactis* ssp. *lactis* IL1403. A;Reference number: A86625; MUID:21235186; P Length 535; Best Local Similarity 50.0%; Pred. No. 1e+02; Matches 5; Conservative 5; Mismatch T20445 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 624; Best Local Similarity 60.0%; Pred. No. 1.2e+02; Matches 6; Conservative 2; Mismatches 2; I C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M. Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0; Qy 2 EIVDSASVPET 12 ::| |:|:| Db E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; ( Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Mirandi and analysis of chromosome 1 of the plant *Arabidopsis*. A;Reference number: A86141; MUID:2101 Conservative 2; Mismatches 4; Indels 0; Gaps 0; Qy 1 NEIVDSASVPET 12 | : : |||| Db 676 NSVAE Protein Sequence Database, November 1999 A;Reference number: Z23023 A;Accession: T46116 A 1229; Best Local Similarity 80.0%; Pred. No. 2.6e+02; Matches 8; Conservative 0; Mismatches 2; C1orf9 gene encodes a putative transmembrane member of a novel protein family. A;Reference nu Length 1254; Best Local Similarity 66.7%; Pred. No. 2.6e+02; Matches 6; Conservative 3; Mismatch A;Description: Molecular cloning and tissue-specific expression of the mutator2 gene (*mu2*) in *Dros* 60.3%; Score 35; DB 2; Length 1261; Best Local Similarity 58.3%; Pred. No. 2.6e+02; Matches 7, heterodimeric coiled-coil protein required for mitotic chromosome condensation in vitro. A;Referenc 60.3%; Score 35; DB 2; Length 1290; Best Local Similarity 63.6%; Pred. No. 2.7e+02; Matches 7, Warrener, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R A82950; MUID:20437337; PMID:10984043 A;Accession: C83269 A;Status: preliminary A;Molecule Gaps 0; Qy 2 EIVDSASVPET 12 |:|: || ||| Db 93 ELVELASQPET 103 RESULT 37 D87150 polypeptide K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Lacroix, C PMID:11234002 A;Accession: D87150 A;Status: preliminary A;Molecule type: DNA A;Residues: 1- NPILETSEIPET 95 RESULT 38 T21655 hypothetical protein F32D8.5a - *Caenorhabditis elegans* C;Sp UNIPARC:UPI0000077CDE; EMBL:Z74031; PIDN:CAA98457.1; GSPDB:GN00023; CESP:F32D8.5a , *Methanobacterium thermoautotrophicum* (strain Delta H) C;Species: *Methanobacterium thermoaut* A.; Bush, D.; Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.; Petrokov shown A;Molecule type: DNA A;Residues: 1-226 A;Cross-references: UNIPROT:O26767; UNIPARC: hypothetical protein F32D8.5b - *Caenorhabditis elegans* C;Species: *Caenorhabditis elegans* C;Date GSPDB:GN00023; CESP:F32D8.5b A;Experimental source: clone F32D8 C;Genetics: A;Gene: CESP A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120 C;Date: 14-Dec 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana* Score 34; DB 2; Length 291; Best Local Similarity 66.7%; Pred. No. 79; Matches 6; Conservative 2 Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Che D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.;

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_263\_274.rup.

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This page gives you Search Results detail for the Application 10616279 and Search Result us-10-616-279-2\_copy\_263\_274.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 123.13 Seconds  
(without alignments)  
90.150 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_263\_274  
Perfect score: 58  
Sequence: 1 NEIVDSASVPET 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	58	100.0	331	1 SPON2_HUMAN	Q9bud6 homo sapien
2	58	100.0	331	2 Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	58	100.0	331	2 Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	53	91.4	129	2 Q3TEM5_MOUSE	Q3tem5 mus musculu



5	53	91.4	289	2	Q6KAS6_MOUSE	Q6kas6	mus musculu
6	53	91.4	330	1	SPON2_MOUSE	Q8bms2	mus musculu
7	53	91.4	330	1	SPON2_RAT	Q9wv75	rattus norv
8	53	91.4	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
9	41	70.7	637	2	Q4ZN61_PSEU2	Q4zn61	pseudomonas
10	40	69.0	304	2	Q58Z28_LACRH	Q58z28	lactobacill
11	40	69.0	429	2	Q5WM20_BACSK	Q5wm20	bacillus cl
12	40	69.0	999	2	Q4Q5S1_LEIMA	Q4q5s1	leishmania
13	39	67.2	157	2	Q8DTK7_STRMU	Q8dtk7	streptococc
14	39	67.2	242	2	Q94MR8_9CAUD	Q94mr8	bacterioph
15	39	67.2	304	2	Q58Z11_LACRH	Q58z11	lactobacill
16	39	67.2	651	2	Q3UTY5_MOUSE	Q3uty5	mus musculu
17	39	67.2	680	2	Q8JZW6_MOUSE	Q8jzw6	mus musculu
18	39	67.2	681	2	Q3UWJ5_MOUSE	Q3uwj5	mus musculu
19	39	67.2	776	2	Q7VH62_HELHP	Q7vh62	helicobacte
20	39	67.2	972	2	Q8CDM3_MOUSE	Q8cdm3	mus musculu
21	39	67.2	1001	1	RPGR_MOUSE	Q9r0x5	mus musculu
22	38	65.5	226	2	Q5C6R8_SCHJA	Q5c6r8	schistosoma
23	38	65.5	323	2	Q6AAP3_PROAC	Q6aap3	propionibac
24	38	65.5	370	2	Q754K6_ASHGO	Q754k6	ashbya goss
25	38	65.5	440	2	Q39AG5_BURS3	Q39ag5	burkholderi
26	38	65.5	441	2	Q7MUI5_PORGI	Q7mui5	porphyromon
27	38	65.5	537	2	Q7UXT4_RHOBA	Q7uxt4	rhodopirell
28	38	65.5	928	2	Q8H7U0_ORYSA	Q8h7u0	oryza sativ
29	38	65.5	1102	1	RPOB_SYNY3	P77965	synechocyst
30	38	65.5	1736	2	Q9C2J9_NEUCR	Q9c2j9	neurospora
31	37	63.8	210	2	Q4HJ72_CAMLA	Q4hj72	campylobact
32	37	63.8	221	2	Q62PK9_BACLD	Q62pk9	bacillus li
33	37	63.8	222	2	Q65E37_BACLD	Q65e37	bacillus li
34	37	63.8	271	2	Q4Q7J3_LEIMA	Q4q7j3	leishmania
35	37	63.8	287	1	H1_LYCES	P37218	lycopersico
36	37	63.8	339	2	Q62IN2_BURMA	Q62in2	burkholderi
37	37	63.8	339	2	Q63VN6_BURPS	Q63vn6	burkholderi
38	37	63.8	360	2	Q3JUB2_BURP1	Q3jub2	burkholderi
39	37	63.8	365	2	Q6BMR8_DEBHA	Q6bmr8	debaryomyce
40	37	63.8	395	2	Q8Y3L1_LISMO	Q8y3l1	listeria mo
41	37	63.8	395	2	Q926T4_LISIN	Q926t4	listeria in
42	37	63.8	403	2	Q4EH56_LISMO	Q4eh56	listeria mo
43	37	63.8	403	2	Q4ET80_LISMO	Q4et80	listeria mo
44	37	63.8	403	2	Q71VT7_LISMF	Q71vt7	listeria mo
45	37	63.8	404	2	Q65NV4_BACLD	Q65nv4	bacillus li
46	37	63.8	446	2	Q3RPS7_RALME	Q3rps7	ralstonia m
47	37	63.8	471	2	Q2X1V8_9GAMM	Q2x1v8	shewanella
48	37	63.8	471	2	Q2ZMR5_SHEPU	Q2zmr5	shewanella
49	37	63.8	512	2	Q7PV52_ANOGA	Q7pv52	anopheles g
50	37	63.8	526	2	Q3E6N1_CHLAU	Q3e6n1	chloroflexu
51	37	63.8	549	2	Q4QBQ6_LEIMA	Q4qbq6	leishmania
52	37	63.8	570	2	Q6JU00_BRARE	Q6juu0	brachydanio
53	37	63.8	570	2	Q6NW58_BRARE	Q6nw58	brachydanio
54	37	63.8	578	2	Q4I1N5_GIBZE	Q4iln5	gibberella
55	37	63.8	593	2	Q3APX5_CHLCH	Q3apx5	chlorobium
56	37	63.8	608	2	Q582I4_9TRYP	Q582i4	trypanosoma
57	37	63.8	653	2	Q5LS11_SILPO	Q5ls11	silicibacte
58	37	63.8	766	2	Q7RI66_PLAYO	Q7ri66	plasmodium
59	37	63.8	810	2	Q5AZL4_EMENI	Q5azl4	aspergillus
60	37	63.8	1039	1	Y304_TREPA	O83326	treponema p
61	37	63.8	1099	2	O68840_BACST	O68840	bacillus st
62	37	63.8	1157	2	Q7RQN5_PLAYO	Q7rqn5	plasmodium
63	37	63.8	1928	2	Q6VZJ3_CNPV	Q6vzj3	canarypox v
64	37	63.8	3971	2	Q6VMD5_9CORO	Q6vmd5	infectious
65	37	63.8	6646	2	Q6VMD6_9CORO	Q6vmd6	infectious

## SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279- 2\_copy\_28\_46.rag.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10616279 and Search Result us-10-616-279-2\_copy\_28\_46.rag.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:19 ; Search time 152.413 Seconds  
(without alignments)  
56.997 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	19	4	AAB82473	Aab82473 Human ext
2	99	100.0	19	9	ADW76927	Adw76927 Human RG1
3	99	100.0	105	3	AAB34693	Aab34693 Human sec
4	99	100.0	331	4	AAB82472	Aab82472 Human ext
5	99	100.0	331	9	ADW76921	Adw76921 Human RG1
6	91	91.9	290	8	ADT50847	Adt50847 Cancer re
7	91	91.9	298	8	ADT50840	Adt50840 Cancer re
8	91	91.9	330	4	AAE12304	Aae12304 Human NPG
9	91	91.9	331	2	AAW70589	Aaw70589 Adhesion-
10	91	91.9	331	2	AAV41721	Aay41721 Human PRO
11	91	91.9	331	3	AAB33465	Aab33465 Human PRO
12	91	91.9	331	3	AAV79561	Aay79561 Cancer sp
13	91	91.9	331	3	AAB44277	Aab44277 Human PRO
14	91	91.9	331	3	AAV95349	Aay95349 Human PRO
15	91	91.9	331	4	AAM93266	Aam93266 Human pol
16	91	91.9	331	4	AAM93324	Aam93324 Human pol
17	91	91.9	331	4	AAM38872	Aam38872 Human pol
18	91	91.9	331	5	ABG61806	Abg61806 Prostate
19	91	91.9	331	5	AAU79944	Aau79944 Human Spo
20	91	91.9	331	5	ABB77393	Abb77393 Human spo
21	91	91.9	331	5	AAE20463	Aae20463 Human tum
22	91	91.9	331	6	ABO25223	Abo25223 Novel hum
23	91	91.9	331	6	ABU72229	Abu72229 Novel hum
24	91	91.9	331	6	ABU84909	Abu84909 Human sec
25	91	91.9	331	6	ABU61107	Abu61107 Human PRO
26	91	91.9	331	6	ABU80376	Abu80376 Human sec
27	91	91.9	331	6	ABG75949	Abg75949 Human ant
28	91	91.9	331	6	ADA24775	Ada24775 Novel hum
29	91	91.9	331	6	ABO19678	Abo19678 Novel hum
30	91	91.9	331	6	ADA12436	Ada12436 Human sec
31	91	91.9	331	6	ABO19569	Abo19569 Novel hum
32	91	91.9	331	7	ADB73742	Adb73742 Human PRO
33	91	91.9	331	7	ADB76458	Adb76458 Human PRO
34	91	91.9	331	7	ADB75561	Adb75561 Prostate
35	91	91.9	331	7	ADC43884	Adc43884 Human sec
36	91	91.9	331	7	ADC61644	Adc61644 Human sec
37	91	91.9	331	7	ADC63608	Adc63608 Human sec
38	91	91.9	331	7	ADC66708	Adc66708 Human sec
39	91	91.9	331	7	ADC68832	Adc68832 Human sec
40	91	91.9	331	7	ADC62892	Adc62892 Human sec
41	91	91.9	331	7	ADC67957	Adc67957 Human sec
42	91	91.9	331	7	ADC41277	Adc41277 Human sec
43	91	91.9	331	7	ADC67332	Adc67332 Human sec
44	91	91.9	331	7	ADC62268	Adc62268 Human sec
45	91	91.9	331	7	ADC41901	Adc41901 Human sec
46	91	91.9	331	7	ADE49270	Ade49270 Human sec
47	91	91.9	331	7	ADE35324	Ade35324 Human sec
48	91	91.9	331	7	ADE16438	Ade16438 Human sec
49	91	91.9	331	7	ADD73053	Add73053 Human sec
50	91	91.9	331	7	ADD72411	Add72411 Human sec
51	91	91.9	331	7	ADE17062	Ade17062 Human sec
52	91	91.9	331	7	ADF47076	Adf47076 Human sec
53	91	91.9	331	7	ADG42579	Adg42579 Novel hum
54	91	91.9	331	7	ADG42585	Adg42585 Human ext
55	91	91.9	331	7	ADG42587	Adg42587 Human ext
56	91	91.9	331	7	ADG52833	Adg52833 Human sec
57	91	91.9	331	7	ADG60153	Adg60153 Human sec

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_28\_46.ra1.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 39.2391 Seconds  
(without alignments)  
42.383 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					
No.	Score	Match	Length	ID		Description

1	99	100.0	19	2	US-09-732-357B-8	Sequence 8, Appli
2	99	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
3	91	91.9	330	2	US-09-371-696-2	Sequence 2, Appli
4	91	91.9	331	2	US-09-949-002-397	Sequence 397, App
5	91	91.9	331	2	US-09-999-833A-236	Sequence 236, App
6	91	91.9	331	2	US-09-807-200-2	Sequence 2, Appli
7	91	91.9	331	2	US-10-020-445A-236	Sequence 236, App
8	91	91.9	331	2	US-09-978-189-236	Sequence 236, App
9	91	91.9	331	2	US-10-017-085A-236	Sequence 236, App
10	91	91.9	331	3	US-10-145-129A-236	Sequence 236, App
11	91	91.9	331	3	US-10-013-929A-236	Sequence 236, App
12	91	91.9	331	3	US-10-013-917A-236	Sequence 236, App
13	91	91.9	422	2	US-09-949-002-504	Sequence 504, App
14	81	81.8	331	1	US-08-799-173A-2	Sequence 2, Appli
15	81	81.8	331	2	US-09-170-042A-2	Sequence 2, Appli
16	69	69.7	330	2	US-09-732-357B-13	Sequence 13, Appl
17	50	50.5	1245	2	US-09-252-991A-30935	Sequence 30935, A
18	46	46.5	545	2	US-09-303-518D-54	Sequence 54, Appl
19	45	45.5	287	2	US-09-252-991A-29808	Sequence 29808, A
20	45	45.5	296	2	US-09-328-352-5366	Sequence 5366, Ap
21	44	44.4	559	2	US-09-252-991A-18444	Sequence 18444, A
22	43.5	43.9	237	2	US-09-902-540-15928	Sequence 15928, A
23	43.5	43.9	917	2	US-09-049-698-41	Sequence 41, Appl
24	43.5	43.9	919	2	US-09-991-181-379	Sequence 379, App
25	43.5	43.9	919	2	US-09-990-444-379	Sequence 379, App
26	43.5	43.9	919	2	US-09-997-333-379	Sequence 379, App
27	43.5	43.9	919	2	US-09-992-598-379	Sequence 379, App
28	43.5	43.9	919	2	US-09-989-735-379	Sequence 379, App
29	43.5	43.9	919	3	US-09-989-726-379	Sequence 379, App
30	43.5	43.9	919	3	US-09-997-514-379	Sequence 379, App
31	43.5	43.9	919	3	US-09-989-728-379	Sequence 379, App
32	43.5	43.9	919	3	US-09-997-349-379	Sequence 379, App
33	43.5	43.9	919	3	US-09-997-653-379	Sequence 379, App
34	43.5	43.9	919	3	US-09-989-293A-379	Sequence 379, App
35	43	43.4	125	2	US-10-094-749-2318	Sequence 2318, Ap
36	43	43.4	336	1	US-08-997-080-156	Sequence 156, App
37	43	43.4	336	1	US-08-997-362-156	Sequence 156, App
38	43	43.4	336	2	US-09-095-855-156	Sequence 156, App
39	42	42.4	137	2	US-09-252-991A-30971	Sequence 30971, A
40	42	42.4	159	2	US-09-621-976-5542	Sequence 5542, Ap
41	42	42.4	258	2	US-09-579-845-8	Sequence 8, Appli
42	42	42.4	275	2	US-09-510-322A-10	Sequence 10, Appl
43	42	42.4	276	2	US-09-514-768B-10	Sequence 10, Appl
44	41	41.4	168	2	US-09-489-039A-11028	Sequence 11028, A
45	41	41.4	197	2	US-09-252-991A-30299	Sequence 30299, A
46	41	41.4	258	2	US-09-579-845-7	Sequence 7, Appli
47	41	41.4	260	2	US-09-252-991A-21611	Sequence 21611, A
48	41	41.4	428	2	US-10-332-795-15	Sequence 15, Appl
49	41	41.4	487	2	US-09-579-845-14	Sequence 14, Appl
50	41	41.4	680	2	US-09-902-540-11278	Sequence 11278, A
51	41	41.4	4302	2	US-09-052-469-8	Sequence 8, Appli
52	41	41.4	4302	2	US-08-422-582-8	Sequence 8, Appli
53	41	41.4	4302	2	US-09-052-262-8	Sequence 8, Appli
54	41	41.4	4339	2	US-09-052-469-6	Sequence 6, Appli
55	41	41.4	4339	2	US-08-422-582-6	Sequence 6, Appli
56	41	41.4	4339	2	US-09-052-262-6	Sequence 6, Appli
57	40.5	40.9	86	2	US-09-252-991A-29178	Sequence 29178, A
58	40	40.4	155	2	US-09-902-540-15567	Sequence 15567, A
59	40	40.4	191	2	US-09-252-991A-18626	Sequence 18626, A
60	40	40.4	355	2	US-09-605-703B-860	Sequence 860, App

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279- 2\_copy\_28\_46.rapbn.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10616279 and Search Result us-10-616-279-2\_copy\_28\_46.rapbn.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 8.26087 Seconds  
(without alignments)  
25.616 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	43.5	43.9	917	7	US-11-302-678-32	Sequence 32, Appl
2	43.5	43.9	919	6	US-10-196-749-258	Sequence 258, App
3	43.5	43.9	919	7	US-11-101-316-70	Sequence 70, Appl
4	39.5	39.9	4074	6	US-10-501-834-2	Sequence 2, Appli
5	39	39.4	137	6	US-10-953-349-6725	Sequence 6725, Ap
6	39	39.4	183	6	US-10-953-349-6724	Sequence 6724, Ap
7	39	39.4	244	6	US-10-953-349-6723	Sequence 6723, Ap
8	39	39.4	327	6	US-10-953-349-8753	Sequence 8753, Ap
9	39	39.4	391	6	US-10-953-349-8752	Sequence 8752, Ap
10	39	39.4	476	6	US-10-953-349-8751	Sequence 8751, Ap
11	39	39.4	582	7	US-11-293-697-3683	Sequence 3683, Ap
12	39	39.4	1912	6	US-10-511-937-2561	Sequence 2561, Ap
13	38	38.4	159	6	US-10-953-349-37541	Sequence 37541, A
14	38	38.4	258	6	US-10-953-349-37540	Sequence 37540, A
15	38	38.4	278	6	US-10-953-349-37539	Sequence 37539, A
16	38	38.4	514	7	US-11-121-154-148	Sequence 148, App
17	37	37.4	177	7	US-11-293-697-4391	Sequence 4391, Ap
18	37	37.4	416	6	US-10-502-993-2	Sequence 2, Appli
19	36.5	36.9	159	7	US-11-293-697-2919	Sequence 2919, Ap
20	36	36.4	71	6	US-10-953-349-25287	Sequence 25287, A
21	36	36.4	71	6	US-10-953-349-26349	Sequence 26349, A
22	36	36.4	91	6	US-10-953-349-29384	Sequence 29384, A
23	36	36.4	161	7	US-11-293-697-3409	Sequence 3409, Ap
24	36	36.4	185	6	US-10-953-349-25898	Sequence 25898, A
25	36	36.4	201	6	US-10-953-349-17374	Sequence 17374, A
26	36	36.4	300	6	US-10-953-349-28850	Sequence 28850, A
27	36	36.4	511	6	US-10-953-349-6576	Sequence 6576, Ap
28	36	36.4	593	6	US-10-953-349-6575	Sequence 6575, Ap
29	36	36.4	632	6	US-10-953-349-9560	Sequence 9560, Ap
30	36	36.4	729	6	US-10-953-349-9559	Sequence 9559, Ap
31	36	36.4	746	6	US-10-953-349-6574	Sequence 6574, Ap
32	36	36.4	794	6	US-10-953-349-9558	Sequence 9558, Ap
33	35.5	35.9	272	7	US-11-293-697-3682	Sequence 3682, Ap
34	35.5	35.9	4059	6	US-10-501-834-6	Sequence 6, Appli
35	35	35.4	114	6	US-10-511-937-2537	Sequence 2537, Ap
36	35	35.4	143	7	US-11-293-697-2546	Sequence 2546, Ap
37	35	35.4	151	7	US-11-293-697-2514	Sequence 2514, Ap
38	35	35.4	154	6	US-10-953-349-21337	Sequence 21337, A
39	35	35.4	197	6	US-10-953-349-40189	Sequence 40189, A
40	35	35.4	208	6	US-10-953-349-2628	Sequence 2628, Ap
41	35	35.4	210	6	US-10-953-349-2627	Sequence 2627, Ap
42	35	35.4	252	6	US-10-953-349-24464	Sequence 24464, A
43	35	35.4	258	6	US-10-953-349-34274	Sequence 34274, A
44	35	35.4	284	6	US-10-953-349-21336	Sequence 21336, A
45	35	35.4	294	6	US-10-953-349-21335	Sequence 21335, A
46	35	35.4	323	7	US-11-293-697-4546	Sequence 4546, Ap
47	35	35.4	332	6	US-10-953-349-28795	Sequence 28795, A
48	35	35.4	349	6	US-10-953-349-14110	Sequence 14110, A
49	35	35.4	355	6	US-10-953-349-14109	Sequence 14109, A
50	35	35.4	362	6	US-10-953-349-14108	Sequence 14108, A
51	35	35.4	362	6	US-10-953-349-28794	Sequence 28794, A
52	35	35.4	419	6	US-10-953-349-16414	Sequence 16414, A
53	35	35.4	448	7	US-11-293-697-4755	Sequence 4755, Ap
54	35	35.4	450	6	US-10-953-349-32232	Sequence 32232, A
55	35	35.4	456	6	US-10-953-349-16413	Sequence 16413, A
56	35	35.4	1023	7	US-11-293-697-3123	Sequence 3123, Ap
57	35	35.4	2026	6	US-10-505-928-831	Sequence 831, App
58	35	35.4	4391	7	US-11-183-325-56	Sequence 56, Appl
59	34.5	34.8	112	6	US-10-953-349-19708	Sequence 19708, A

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_28\_46.rapbm.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 137.13 Seconds  
(without alignments)  
64.180 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
-----				



1	99	100.0	19	3	US-09-732-357A-8	Sequence 8, Appli
2	99	100.0	19	4	US-10-616-279-8	Sequence 8, Appli
3	99	100.0	19	4	US-10-624-884-8	Sequence 8, Appli
4	99	100.0	19	5	US-10-895-183-8	Sequence 8, Appli
5	99	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
6	99	100.0	331	4	US-10-616-279-2	Sequence 2, Appli
7	99	100.0	331	4	US-10-624-884-2	Sequence 2, Appli
8	99	100.0	331	5	US-10-895-183-2	Sequence 2, Appli
9	91	91.9	330	3	US-09-903-383-2	Sequence 2, Appli
10	91	91.9	331	3	US-09-978-295A-236	Sequence 236, App
11	91	91.9	331	3	US-09-938-418-8	Sequence 8, Appli
12	91	91.9	331	3	US-09-978-697-236	Sequence 236, App
13	91	91.9	331	3	US-09-978-192A-236	Sequence 236, App
14	91	91.9	331	3	US-09-999-832A-236	Sequence 236, App
15	91	91.9	331	3	US-09-978-189-236	Sequence 236, App
16	91	91.9	331	3	US-09-978-608A-236	Sequence 236, App
17	91	91.9	331	3	US-09-978-585A-236	Sequence 236, App
18	91	91.9	331	3	US-09-978-191A-236	Sequence 236, App
19	91	91.9	331	3	US-09-978-403A-236	Sequence 236, App
20	91	91.9	331	3	US-09-978-564A-236	Sequence 236, App
21	91	91.9	331	3	US-09-999-833A-236	Sequence 236, App
22	91	91.9	331	3	US-09-981-915A-236	Sequence 236, App
23	91	91.9	331	3	US-09-978-824-236	Sequence 236, App
24	91	91.9	331	3	US-09-918-585A-236	Sequence 236, App
25	91	91.9	331	3	US-09-999-834A-236	Sequence 236, App
26	91	91.9	331	3	US-09-978-423A-236	Sequence 236, App
27	91	91.9	331	3	US-09-978-193A-236	Sequence 236, App
28	91	91.9	331	3	US-09-999-830A-236	Sequence 236, App
29	91	91.9	331	3	US-09-978-757A-236	Sequence 236, App
30	91	91.9	331	3	US-09-978-187B-236	Sequence 236, App
31	91	91.9	331	3	US-09-978-643A-236	Sequence 236, App
32	91	91.9	331	3	US-09-978-375A-236	Sequence 236, App
33	91	91.9	331	3	US-09-978-298A-236	Sequence 236, App
34	91	91.9	331	3	US-09-978-188A-236	Sequence 236, App
35	91	91.9	331	3	US-09-978-681A-236	Sequence 236, App
36	91	91.9	331	3	US-09-978-194A-236	Sequence 236, App
37	91	91.9	331	3	US-09-999-829A-236	Sequence 236, App
38	91	91.9	331	3	US-09-978-299A-236	Sequence 236, App
39	91	91.9	331	3	US-09-978-544A-236	Sequence 236, App
40	91	91.9	331	3	US-09-978-665A-236	Sequence 236, App
41	91	91.9	331	3	US-09-978-802A-236	Sequence 236, App
42	91	91.9	331	3	US-09-970-944-12	Sequence 12, Appl
43	91	91.9	331	3	US-09-970-944-38	Sequence 38, Appl
44	91	91.9	331	3	US-09-970-944-40	Sequence 40, Appl
45	91	91.9	331	3	US-09-999-831A-236	Sequence 236, App
46	91	91.9	331	3	US-09-978-824-236	Sequence 236, App
47	91	91.9	331	4	US-10-017-081A-236	Sequence 236, App
48	91	91.9	331	4	US-10-167-749-236	Sequence 236, App
49	91	91.9	331	4	US-10-013-921A-236	Sequence 236, App
50	91	91.9	331	4	US-10-013-929A-236	Sequence 236, App
51	91	91.9	331	4	US-10-016-177A-236	Sequence 236, App
52	91	91.9	331	4	US-10-166-709A-236	Sequence 236, App
53	91	91.9	331	4	US-10-205-823-385	Sequence 385, App
54	91	91.9	331	4	US-10-143-031A-236	Sequence 236, App
55	91	91.9	331	4	US-10-143-030A-236	Sequence 236, App
56	91	91.9	331	4	US-10-002-967A-236	Sequence 236, App
57	91	91.9	331	4	US-10-017-083A-236	Sequence 236, App
58	91	91.9	331	4	US-10-145-128A-236	Sequence 236, App
59	91	91.9	331	4	US-10-017-191A-236	Sequence 236, App
60	91	91.9	331	4	US-10-143-028A-236	Sequence 236, App
61	91	91.9	331	4	US-10-143-029A-236	Sequence 236, App

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A;Cross-references: UNIPROT:P95087; UNIPARC:UPI0000165332; GB:Z83866; GB:AL123456; NII  
membrane efflux protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-  
PIDN:CAB51438.1; GSPDB:GN00070; SCOEDB:SC4G6.15c A;Experimental source: strain A3(2) C;

GenCore version 5.1.8

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:36:56 ; Search time 23.9565 Seconds  
(without alignments)  
76.310 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	50.5	851	2	A83484	probable heme util
2	46	46.5	176	2	B81208	conserved hypothet
3	46	46.5	545	2	D81973	probable integral
4	45	45.5	273	2	B83551	hypothetical prote
5	44	44.4	3227	2	T37964	probable ubiquitin

6	43	43.4	25	2	S44201	HLA-DRB1 exon2 pro
7	43	43.4	277	2	S71222	xyloglucan endo-1,
8	42	42.4	156	2	A70412	hypothetical prote
9	42	42.4	263	1	KYRTB	chymotrypsin (EC 3
10	42	42.4	416	2	S52078	prostacyclin - rat
11	42	42.4	1465	2	S43529	165K protein, skel
12	41.5	41.9	245	2	S56827	conserved hypothet
13	41.5	41.9	459	2	T19110	hypothetical prote
14	41.5	41.9	521	2	T18942	3-oxoacid CoA-tran
15	41.5	41.9	790	2	H71509	phenylalanine-tRNA
16	41	41.4	99	2	H86480	10.9K hypothetical
17	41	41.4	134	2	B69156	hypothetical prote
18	41	41.4	413	2	G87299	poly A polymerase
19	41	41.4	455	2	AH2055	hypothetical prote
20	41	41.4	457	2	B87269	hypothetical prote
21	41	41.4	4302	2	A38971	polycystic kidney
22	40.5	40.9	493	2	C97605	probable serine pr
23	40.5	40.9	514	2	AE2827	serine proteinase
24	40	40.4	302	2	T50737	bacteriochlorophyl
25	40	40.4	387	2	F69304	3-ketoacyl-CoA thi
26	40	40.4	417	2	A54416	prostacyclin recep
27	40	40.4	460	2	T19111	hypothetical prote
28	40	40.4	475	2	S73746	MG294 homolog A05_
29	40	40.4	1290	2	T00018	period protein hom
30	40	40.4	1333	2	S65812	RNA-directed DNA p
31	39.5	39.9	236	2	F83083	hypothetical prote
32	39.5	39.9	367	2	B72644	probable transketo
33	39.5	39.9	387	2	AI3003	amidohydrolase [im
34	39.5	39.9	430	2	H98279	probable hydrolase
35	39.5	39.9	615	2	D83315	NADH2 dehydrogenas
36	39	39.4	68	2	T09545	metallothionein-li
37	39	39.4	108	1	KVMS09	Ig kappa chain V r
38	39	39.4	166	2	F82774	hypothetical prote
39	39	39.4	188	2	AC3613	probable s-adenosy
40	39	39.4	219	2	T09671	RPE15 protein - al
41	39	39.4	234	2	F46449	hypothetical prote
42	39	39.4	245	1	KYBOB	chymotrypsin (EC 3
43	39	39.4	295	2	C95354	probable epimerase
44	39	39.4	299	2	S60971	probable membrane
45	39	39.4	308	2	S44818	F44E2.8 protein -
46	39	39.4	329	2	AC3640	FMN adenylyltransf
47	39	39.4	329	2	B83162	molybdopterin bios
48	39	39.4	368	2	D72606	hypothetical prote
49	39	39.4	369	2	H70650	hypothetical prote
50	39	39.4	384	2	T35075	probable integral
51	39	39.4	402	2	T04348	endosperm specific
52	39	39.4	430	2	AB3147	conserved hypothet
53	39	39.4	430	2	H98140	hypothetical prote
54	39	39.4	447	2	T05003	hypothetical prote
55	39	39.4	461	2	A70837	probable proteinas
56	39	39.4	465	2	T19113	hypothetical prote
57	39	39.4	492	1	A27727	trypanothione-disu
58	39	39.4	522	2	T28113	hypothetical prote
59	39	39.4	585	2	B49596	genome polyprotein
60	39	39.4	677	2	E70722	hypothetical prote
61	39	39.4	1067	1	S62421	endopeptidase La h
62	39	39.4	1612	2	T30805	dutt1 protein - mo
63	39	39.4	1651	2	T14160	transmembrane rece
64	38.5	38.9	164	2	E75062	probable flagella-
65	38.5	38.9	681	2	AD3318	DNA primase (EC 2.
66	38	38.4	133	2	C31211	T-cell receptor be

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_28\_46.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 194.957 Seconds  
(without alignments)  
90.150 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_28\_46  
Perfect score: 99  
Sequence: 1 PLGGESICSAGAPAKYSIT 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	91	91.9	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	81	81.8	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	75	75.8	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	69	69.7	330	1	SPON2_MOUSE	Q8bms2 mus musculu

5	69	69.7	330	1	SPON2_RAT	Q9wv75	rattus norv
6	69	69.7	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
7	51	51.5	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
8	51	51.5	1450	2	Q4SCT9_TETNG	Q4sct9	tetraodon n
9	50	50.5	606	2	Q2KF89_MAGGR	Q2kf89	magnaporthe
10	50	50.5	851	2	Q9I442_PSEAE	Q9i442	pseudomonas
11	49	49.5	269	2	Q66IB2_BRARE	Q66ib2	brachydanio
12	49	49.5	412	2	Q501Z8_BRARE	Q501z8	brachydanio
13	49	49.5	532	2	Q6CE62_YARLI	Q6ce62	yarrowia li
14	49	49.5	553	2	Q95PZ3_CAEEL	Q95pz3	caenorhabdi
15	48	48.5	456	2	Q44K09_CHRSL	Q44k09	chromohalob
16	48	48.5	765	2	Q7UBR0_SHIFL	Q7ubr0	shigella fl
17	48	48.5	765	2	Q83JU7_SHIFL	Q83ju7	shigella fl
18	48	48.5	928	2	Q32LP3_BOVIN	Q32lp3	bos taurus
19	48	48.5	991	2	Q94C44_CHLRE	Q94c44	chlamydomon
20	48	48.5	1021	2	Q5P6N2_AZOSE	Q5p6n2	azoarcus sp
21	48	48.5	1463	2	O55124_MOUSE	O55124	mus musculu
22	48	48.5	1463	2	Q3UQS9_MOUSE	Q3uqs9	mus musculu
23	48	48.5	2368	2	Q4S4K5_TETNG	Q4s4k5	tetraodon n
24	47	47.5	185	2	Q63TB9_BURPS	Q63tb9	burkholderi
25	47	47.5	284	2	Q37KV3_RHOPA	Q37kv3	rhodopseudo
26	47	47.5	321	2	Q2IID2_9DELT	Q2iid2	anaeromyxob
27	47	47.5	345	2	Q7VVT4_BORPE	Q7vvt4	bordetella
28	47	47.5	345	2	Q7WKN6_BORBR	Q7wkn6	bordetella
29	47	47.5	875	2	Q4HU86_GIBZE	Q4hu86	gibberella
30	47	47.5	1261	2	Q7S3G2_NEUCR	Q7s3g2	neurospora
31	47	47.5	1286	2	Q4P188_USTMA	Q4p188	ustilago ma
32	46.5	47.0	1258	2	Q4S9F0_TETNG	Q4s9f0	tetraodon n
33	46	46.5	176	2	Q5F6F3_NEIG1	Q5f6f3	neisseria g
34	46	46.5	176	2	Q7DDQ9_NEIMB	Q7ddq9	neisseria m
35	46	46.5	176	2	Q9JRC8_NEIMA	Q9jrc8	neisseria m
36	46	46.5	214	2	Q3J230_RHOS4	Q3j230	rhodobacter
37	46	46.5	514	2	Q2RQ6_RHORU	Q2rq6	rhodospiril
38	46	46.5	545	1	OXAA_NEIMA	Q9jw48	neisseria m
39	46	46.5	545	2	Q5F4W6_NEIG1	Q5f4w6	neisseria g
40	46	46.5	769	2	Q3E2U2_CHLAU	Q3e2u2	chloroflexu
41	46	46.5	1278	2	Q4BAZ6_BURVI	Q4baz6	burkholderi
42	45.5	46.0	340	2	Q922N8_MOUSE	Q922n8	mus musculu
43	45.5	46.0	402	2	Q3FZ78_9DELT	Q3fz78	pelobacter
44	45.5	46.0	612	2	Q7TPN9_MOUSE	Q7tpn9	m cdna sequ
45	45	45.5	144	2	Q3UGU2_MOUSE	Q3ugu2	mus musculu
46	45	45.5	250	2	Q4RVC6_TETNG	Q4rvc6	tetraodon n
47	45	45.5	258	2	Q4Q386_LEIMA	Q4q386	leishmania
48	45	45.5	273	2	Q9I5I0_PSEAE	Q9i5i0	pseudomonas
49	45	45.5	282	2	Q2WGE5_SELUN	Q2wge5	selaginella
50	45	45.5	335	2	Q2RRN6_RHORU	Q2rrn6	rhodospiril
51	45	45.5	384	1	MAPK3_BOVIN	Q3sy22	bos taurus
52	45	45.5	472	2	Q478P4_DECAR	Q478p4	dechloromon
53	45	45.5	503	2	Q2RWD0_RHORU	Q2rwd0	rhodospiril
54	45	45.5	593	2	Q4Q537_LEIMA	Q4q537	leishmania
55	45	45.5	885	2	Q4Q533_LEIMA	Q4q533	leishmania
56	45	45.5	1051	2	Q440L1_SOLUS	Q440l1	solibacter
57	45	45.5	1285	2	Q8K3T3_SPAJD	Q8k3t3	spalax juda
58	44.5	44.9	259	2	Q4HQQ6_CAMUP	Q4hqq6	campylobact
59	44.5	44.9	304	2	Q4S839_TETNG	Q4s839	tetraodon n
60	44.5	44.9	319	2	Q3B0K9_SYNS9	Q3b0k9	synecococc
61	44.5	44.9	327	2	Q2RTC5_RHORU	Q2rtc5	rhodospiril
62	44.5	44.9	573	2	Q8H7K9_ORYSA	Q8h7k9	oryza sativ
63	44	44.4	89	2	Q69SN1_ORYSA	Q69sn1	oryza sativ
64	44	44.4	209	1	RL19B_ARATH	Q9luq6	arabidopsis
65	44	44.4	265	2	O74696_PHANO	O74696	phaeosphaer

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_77\_91.rag.

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:19 ; Search time 120.326 Seconds  
(without alignments)  
56.997 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85	100.0	15	4	AAB82474	Aab82474 Human ext
2	85	100.0	15	9	ADW76929	Adw76929 Human RG1
3	85	100.0	290	2	AAW83329	Aaw83329 Human min
4	85	100.0	290	8	ADT50847	Adt50847 Cancer re
5	85	100.0	298	8	ADT50840	Adt50840 Cancer re
6	85	100.0	330	4	AAE12304	Aae12304 Human NPG
7	85	100.0	331	2	AAW23663	Aaw23663 Human neu
8	85	100.0	331	2	AAW70589	Aaw70589 Adhesion-
9	85	100.0	331	2	AAW83328	Aaw83328 Human min
10	85	100.0	331	2	AAy41721	Aay41721 Human PRO
11	85	100.0	331	2	AAW92460	Aaw92460 Human NAF
12	85	100.0	331	3	AAB33465	Aab33465 Human PRO
13	85	100.0	331	3	AAy79561	Aay79561 Cancer sp
14	85	100.0	331	3	AAB44277	Aab44277 Human PRO
15	85	100.0	331	3	AAy95349	Aay95349 Human PRO
16	85	100.0	331	4	AAM93266	Aam93266 Human pol
17	85	100.0	331	4	AAM93324	Aam93324 Human pol
18	85	100.0	331	4	AAM38872	Aam38872 Human pol
19	85	100.0	331	4	AAB82472	Aab82472 Human ext
20	85	100.0	331	5	ABG61806	Abg61806 Prostate
21	85	100.0	331	5	AAU79944	Aau79944 Human Spo
22	85	100.0	331	5	ABB77393	Abb77393 Human spo
23	85	100.0	331	5	AAE20463	Aae20463 Human tum
24	85	100.0	331	6	ABO25223	Abo25223 Novel hum
25	85	100.0	331	6	ABU72229	Abu72229 Novel hum
26	85	100.0	331	6	ABU84909	Abu84909 Human sec
27	85	100.0	331	6	ABU61107	Abu61107 Human PRO
28	85	100.0	331	6	ABU80376	Abu80376 Human sec
29	85	100.0	331	6	ABG75949	Abg75949 Human ant
30	85	100.0	331	6	ADA24775	Ada24775 Novel hum
31	85	100.0	331	6	ABO19678	Abo19678 Novel hum
32	85	100.0	331	6	ADA12436	Ada12436 Human sec
33	85	100.0	331	6	ABO19569	Abo19569 Novel hum
34	85	100.0	331	7	ADB73742	Adb73742 Human PRO
35	85	100.0	331	7	ADB76458	Adb76458 Human PRO
36	85	100.0	331	7	ADB75561	Adb75561 Prostate
37	85	100.0	331	7	ADC43884	Adc43884 Human sec
38	85	100.0	331	7	ADC61644	Adc61644 Human sec
39	85	100.0	331	7	ADC63608	Adc63608 Human sec
40	85	100.0	331	7	ADC66708	Adc66708 Human sec
41	85	100.0	331	7	ADC68832	Adc68832 Human sec
42	85	100.0	331	7	ADC62892	Adc62892 Human sec
43	85	100.0	331	7	ADC67957	Adc67957 Human sec
44	85	100.0	331	7	ADC41277	Adc41277 Human sec
45	85	100.0	331	7	ADC67332	Adc67332 Human sec
46	85	100.0	331	7	ADC62268	Adc62268 Human sec
47	85	100.0	331	7	ADC41901	Adc41901 Human sec
48	85	100.0	331	7	ADE49270	Ade49270 Human sec
49	85	100.0	331	7	ADE35324	Ade35324 Human sec
50	85	100.0	331	7	ADE16438	Adel6438 Human sec
51	85	100.0	331	7	ADD73053	Add73053 Human sec
52	85	100.0	331	7	ADD72411	Add72411 Human sec
53	85	100.0	331	7	ADE17062	Adel7062 Human sec
54	85	100.0	331	7	ADF47076	Adf47076 Human sec
55	85	100.0	331	7	ADG42579	Adg42579 Novel hum
56	85	100.0	331	7	ADG42585	Adg42585 Human ext
57	85	100.0	331	7	ADG42586	Adg42586 Human ext

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_77\_91.ra1.

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:44:44 ; Search time 30.9783 Seconds  
(without alignments)  
42.383 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	%
No.	Score	Match Length DB ID
Description		
-----		



1	85	100.0	15	2	US-09-732-357B-10	Sequence 10, Appl
2	85	100.0	330	2	US-09-371-696-2	Sequence 2, Appli
3	85	100.0	331	1	US-08-799-173A-2	Sequence 2, Appli
4	85	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
5	85	100.0	331	2	US-09-170-042A-2	Sequence 2, Appli
6	85	100.0	331	2	US-09-949-002-397	Sequence 397, App
7	85	100.0	331	2	US-09-999-833A-236	Sequence 236, App
8	85	100.0	331	2	US-09-807-200-2	Sequence 2, Appli
9	85	100.0	331	2	US-10-020-445A-236	Sequence 236, App
10	85	100.0	331	2	US-09-978-189-236	Sequence 236, App
11	85	100.0	331	2	US-10-017-085A-236	Sequence 236, App
12	85	100.0	331	3	US-10-145-129A-236	Sequence 236, App
13	85	100.0	331	3	US-10-013-929A-236	Sequence 236, App
14	85	100.0	331	3	US-10-013-917A-236	Sequence 236, App
15	85	100.0	422	2	US-09-949-002-504	Sequence 504, App
16	82	96.5	330	2	US-09-732-357B-13	Sequence 13, Appl
17	52	61.2	299	2	US-09-311-021-202	Sequence 202, App
18	44	51.8	677	2	US-09-270-767-58094	Sequence 58094, A
19	44	51.8	847	2	US-09-270-767-42783	Sequence 42783, A
20	42	49.4	25	2	US-09-270-767-58735	Sequence 58735, A
21	42	49.4	250	2	US-09-248-796A-15562	Sequence 15562, A
22	42	49.4	294	2	US-10-012-231A-123	Sequence 123, App
23	42	49.4	294	2	US-10-015-389A-123	Sequence 123, App
24	42	49.4	294	2	US-10-006-768A-123	Sequence 123, App
25	42	49.4	294	2	US-10-015-671A-123	Sequence 123, App
26	42	49.4	294	2	US-10-015-393A-123	Sequence 123, App
27	42	49.4	294	2	US-10-011-833A-123	Sequence 123, App
28	42	49.4	294	2	US-10-006-041A-123	Sequence 123, App
29	42	49.4	294	2	US-10-012-064A-123	Sequence 123, App
30	42	49.4	294	2	US-10-015-392A-123	Sequence 123, App
31	42	49.4	294	3	US-10-011-795B-123	Sequence 123, App
32	42	49.4	294	3	US-10-015-386A-123	Sequence 123, App
33	42	49.4	294	3	US-10-012-121A-123	Sequence 123, App
34	42	49.4	294	3	US-10-006-485A-123	Sequence 123, App
35	42	49.4	294	3	US-10-006-746A-123	Sequence 123, App
36	42	49.4	294	3	US-10-012-752A-123	Sequence 123, App
37	42	49.4	294	3	US-10-017-253A-123	Sequence 123, App
38	42	49.4	294	3	US-10-015-519A-123	Sequence 123, App
39	42	49.4	294	3	US-10-015-715A-123	Sequence 123, App
40	42	49.4	294	3	US-10-007-236A-123	Sequence 123, App
41	42	49.4	435	2	US-09-072-917A-9	Sequence 9, Appli
42	42	49.4	877	2	US-09-165-396-5	Sequence 5, Appli
43	42	49.4	3129	2	US-09-482-788-2	Sequence 2, Appli
44	41	48.2	149	2	US-09-270-767-47885	Sequence 47885, A
45	41	48.2	297	2	US-09-248-796A-25364	Sequence 25364, A
46	40	47.1	111	2	US-09-248-796A-21330	Sequence 21330, A
47	40	47.1	114	2	US-09-513-999C-5768	Sequence 5768, Ap
48	40	47.1	456	2	US-09-489-039A-8101	Sequence 8101, Ap
49	40	47.1	462	2	US-09-543-681A-5290	Sequence 5290, Ap
50	40	47.1	742	2	US-09-500-123-12	Sequence 12, Appl
51	40	47.1	811	2	US-09-500-123-9	Sequence 9, Appli
52	40	47.1	871	2	US-09-500-123-7	Sequence 7, Appli
53	40	47.1	1008	2	US-09-949-016-10423	Sequence 10423, A
54	39	45.9	152	2	US-09-270-767-37205	Sequence 37205, A
55	39	45.9	152	2	US-09-270-767-52422	Sequence 52422, A
56	39	45.9	163	2	US-09-328-352-7800	Sequence 7800, Ap
57	39	45.9	249	2	US-09-270-767-43254	Sequence 43254, A
58	39	45.9	281	2	US-09-248-796A-23359	Sequence 23359, A
59	39	45.9	635	2	US-09-248-796A-16944	Sequence 16944, A
60	39	45.9	1085	1	US-08-431-080-28	Sequence 28, Appl
61	39	45.9	1085	1	US-08-938-534-28	Sequence 28, Appl

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_77\_91.rapbm.

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:05:59 ; Search time 108.261 Seconds  
(without alignments)  
64.180 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWKRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
-----					

1	85	100.0	15	3	US-09-732-357A-10	Sequence 10, Appl
2	85	100.0	15	4	US-10-616-279-10	Sequence 10, Appl
3	85	100.0	15	4	US-10-624-884-10	Sequence 10, Appl
4	85	100.0	15	5	US-10-895-183-10	Sequence 10, Appl
5	85	100.0	290	4	US-10-629-952-4	Sequence 4, Appli
6	85	100.0	330	3	US-09-903-383-2	Sequence 2, Appli
7	85	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
8	85	100.0	331	3	US-09-978-295A-236	Sequence 236, App
9	85	100.0	331	3	US-09-938-418-8	Sequence 8, Appli
10	85	100.0	331	3	US-09-978-697-236	Sequence 236, App
11	85	100.0	331	3	US-09-978-192A-236	Sequence 236, App
12	85	100.0	331	3	US-09-999-832A-236	Sequence 236, App
13	85	100.0	331	3	US-09-978-189-236	Sequence 236, App
14	85	100.0	331	3	US-09-978-608A-236	Sequence 236, App
15	85	100.0	331	3	US-09-978-585A-236	Sequence 236, App
16	85	100.0	331	3	US-09-978-191A-236	Sequence 236, App
17	85	100.0	331	3	US-09-978-403A-236	Sequence 236, App
18	85	100.0	331	3	US-09-978-564A-236	Sequence 236, App
19	85	100.0	331	3	US-09-999-833A-236	Sequence 236, App
20	85	100.0	331	3	US-09-981-915A-236	Sequence 236, App
21	85	100.0	331	3	US-09-978-824-236	Sequence 236, App
22	85	100.0	331	3	US-09-918-585A-236	Sequence 236, App
23	85	100.0	331	3	US-09-999-834A-236	Sequence 236, App
24	85	100.0	331	3	US-09-978-423A-236	Sequence 236, App
25	85	100.0	331	3	US-09-978-193A-236	Sequence 236, App
26	85	100.0	331	3	US-09-999-830A-236	Sequence 236, App
27	85	100.0	331	3	US-09-978-757A-236	Sequence 236, App
28	85	100.0	331	3	US-09-978-187B-236	Sequence 236, App
29	85	100.0	331	3	US-09-978-643A-236	Sequence 236, App
30	85	100.0	331	3	US-09-978-375A-236	Sequence 236, App
31	85	100.0	331	3	US-09-978-298A-236	Sequence 236, App
32	85	100.0	331	3	US-09-978-188A-236	Sequence 236, App
33	85	100.0	331	3	US-09-978-681A-236	Sequence 236, App
34	85	100.0	331	3	US-09-978-194A-236	Sequence 236, App
35	85	100.0	331	3	US-09-999-829A-236	Sequence 236, App
36	85	100.0	331	3	US-09-978-299A-236	Sequence 236, App
37	85	100.0	331	3	US-09-978-544A-236	Sequence 236, App
38	85	100.0	331	3	US-09-978-665A-236	Sequence 236, App
39	85	100.0	331	3	US-09-978-802A-236	Sequence 236, App
40	85	100.0	331	3	US-09-970-944-12	Sequence 12, Appl
41	85	100.0	331	3	US-09-970-944-38	Sequence 38, Appl
42	85	100.0	331	3	US-09-970-944-39	Sequence 39, Appl
43	85	100.0	331	3	US-09-970-944-40	Sequence 40, Appl
44	85	100.0	331	3	US-09-999-831A-236	Sequence 236, App
45	85	100.0	331	3	US-09-978-824-236	Sequence 236, App
46	85	100.0	331	4	US-10-017-081A-236	Sequence 236, App
47	85	100.0	331	4	US-10-167-749-236	Sequence 236, App
48	85	100.0	331	4	US-10-013-921A-236	Sequence 236, App
49	85	100.0	331	4	US-10-013-929A-236	Sequence 236, App
50	85	100.0	331	4	US-10-016-177A-236	Sequence 236, App
51	85	100.0	331	4	US-10-166-709A-236	Sequence 236, App
52	85	100.0	331	4	US-10-205-823-385	Sequence 385, App
53	85	100.0	331	4	US-10-143-031A-236	Sequence 236, App
54	85	100.0	331	4	US-10-143-030A-236	Sequence 236, App
55	85	100.0	331	4	US-10-002-967A-236	Sequence 236, App
56	85	100.0	331	4	US-10-017-083A-236	Sequence 236, App
57	85	100.0	331	4	US-10-145-128A-236	Sequence 236, App
58	85	100.0	331	4	US-10-017-191A-236	Sequence 236, App
59	85	100.0	331	4	US-10-143-028A-236	Sequence 236, App
60	85	100.0	331	4	US-10-143-029A-236	Sequence 236, App
61	85	100.0	331	4	US-10-145-089A-236	Sequence 236, App

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OM protein - protein search, using sw model

Run on: May 25, 2006, 13:06:00 ; Search time 6.52174 Seconds  
(without alignments)  
25.616 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result    %  
Query

No.	Score	Match	Length	DB	ID	Description
1	42	49.4	294	6	US-10-196-749-278	Sequence 278, App
2	42	49.4	295	1	US-09-949-925-128	Sequence 128, App
3	42	49.4	377	6	US-10-953-349-15715	Sequence 15715, A
4	40	47.1	963	7	US-11-223-738-5	Sequence 5, Appli
5	38	44.7	349	6	US-10-953-349-20252	Sequence 20252, A
6	38	44.7	354	6	US-10-505-928-866	Sequence 866, App
7	38	44.7	405	6	US-10-953-349-960	Sequence 960, App
8	38	44.7	415	6	US-10-953-349-959	Sequence 959, App
9	38	44.7	467	6	US-10-953-349-20251	Sequence 20251, A
10	38	44.7	490	6	US-10-953-349-20250	Sequence 20250, A
11	37	43.5	229	6	US-10-953-349-2040	Sequence 2040, Ap
12	37	43.5	338	6	US-10-953-349-2039	Sequence 2039, Ap
13	37	43.5	340	6	US-10-953-349-2038	Sequence 2038, Ap
14	37	43.5	3460	6	US-10-505-928-104	Sequence 104, App
15	36	42.4	180	6	US-10-953-349-7012	Sequence 7012, Ap
16	36	42.4	186	6	US-10-953-349-23754	Sequence 23754, A
17	36	42.4	298	6	US-10-953-349-7011	Sequence 7011, Ap
18	36	42.4	331	6	US-10-953-349-10129	Sequence 10129, A
19	36	42.4	346	7	US-11-293-697-3812	Sequence 3812, Ap
20	36	42.4	348	6	US-10-953-349-7010	Sequence 7010, Ap
21	36	42.4	587	6	US-10-511-937-2407	Sequence 2407, Ap
22	36	42.4	661	7	US-11-293-697-4325	Sequence 4325, Ap
23	36	42.4	1043	6	US-10-511-937-2452	Sequence 2452, Ap
24	35	41.2	143	6	US-10-953-349-26097	Sequence 26097, A
25	35	41.2	152	6	US-10-953-349-26096	Sequence 26096, A
26	35	41.2	156	6	US-10-953-349-24796	Sequence 24796, A
27	35	41.2	180	6	US-10-953-349-24795	Sequence 24795, A
28	35	41.2	325	7	US-11-293-697-3615	Sequence 3615, Ap
29	35	41.2	354	6	US-10-953-349-23264	Sequence 23264, A
30	35	41.2	365	6	US-10-953-349-15716	Sequence 15716, A
31	35	41.2	417	6	US-10-953-349-1118	Sequence 1118, Ap
32	35	41.2	424	6	US-10-953-349-1117	Sequence 1117, Ap
33	35	41.2	450	6	US-10-953-349-1116	Sequence 1116, Ap
34	35	41.2	485	6	US-10-953-349-11658	Sequence 11658, A
35	35	41.2	603	6	US-10-953-349-11657	Sequence 11657, A
36	35	41.2	703	6	US-10-953-349-11656	Sequence 11656, A
37	35	41.2	956	7	US-11-293-697-3037	Sequence 3037, Ap
38	34	40.0	314	6	US-10-501-834-220	Sequence 220, App
39	34	40.0	316	6	US-10-501-834-221	Sequence 221, App
40	34	40.0	359	6	US-10-953-349-27744	Sequence 27744, A
41	34	40.0	360	6	US-10-953-349-34996	Sequence 34996, A
42	34	40.0	390	6	US-10-953-349-27743	Sequence 27743, A
43	34	40.0	396	1	US-09-949-925-165	Sequence 165, App
44	34	40.0	432	6	US-10-953-349-34995	Sequence 34995, A
45	34	40.0	436	6	US-10-953-349-27742	Sequence 27742, A
46	34	40.0	439	6	US-10-953-349-34994	Sequence 34994, A
47	34	40.0	511	6	US-10-953-349-19020	Sequence 19020, A
48	34	40.0	589	6	US-10-953-349-19019	Sequence 19019, A
49	34	40.0	608	6	US-10-953-349-19018	Sequence 19018, A
50	34	40.0	695	7	US-11-293-697-4190	Sequence 4190, Ap
51	34	40.0	721	7	US-11-293-697-3470	Sequence 3470, Ap
52	33.5	39.4	416	7	US-11-264-784-359	Sequence 359, App
53	33	38.8	193	6	US-10-953-349-32280	Sequence 32280, A
54	33	38.8	200	6	US-10-953-349-32279	Sequence 32279, A
55	33	38.8	259	6	US-10-953-349-3044	Sequence 3044, Ap
56	33	38.8	297	7	US-11-293-697-4132	Sequence 4132, Ap
57	33	38.8	329	6	US-10-953-349-24690	Sequence 24690, A
58	33	38.8	332	6	US-10-953-349-24689	Sequence 24689, A
59	33	38.8	347	6	US-10-953-349-1330	Sequence 1330, Ap

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This page gives you Search Results detail for the Application 10616279 and Search Result us-10-6:  
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:36:56 ; Search time 18.913 Seconds  
(without alignments)  
76.310 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_80:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	54.1	438	1	ALBH	alpha-amylase (EC
2	43.5	51.2	545	2	T40207	hypothetical prote
3	42	49.4	435	2	JC7137	alpha-amylase (EC
4	42	49.4	435	2	S12625	alpha-amylase (EC
5	42	49.4	729	2	C64854	ferric-coprogen re
6	42	49.4	729	2	H90813	outer membrane rec
7	42	49.4	729	2	D85673	outer membrane rec
8	42	49.4	877	2	S58824	probable membrane

9	42	49.4	1080	2	A71485	probable pbp2-tran
10	42	49.4	3587	2	I40486	surfactin syntheta
11	41	48.2	121	2	E97103	hypothetical prote
12	41	48.2	304	2	D82189	conserved hypothet
13	41	48.2	372	2	G89921	alanine dehydrogen
14	41	48.2	410	2	S77661	hypothetical prote
15	41	48.2	432	2	G90268	conserved hypothet
16	41	48.2	805	2	T34212	hypothetical prote
17	40	47.1	135	2	C21826	alpha-amylase (EC
18	40	47.1	153	2	A21826	alpha-amylase (EC
19	40	47.1	299	2	D82880	cytosine-specific
20	40	47.1	337	2	AD3614	glycosyl transfera
21	40	47.1	423	2	T09942	alpha-amylase (EC
22	40	47.1	427	1	ALBHB	alpha-amylase (EC
23	40	47.1	429	1	JE0406	alpha-amylase (EC
24	40	47.1	527	2	A82431	sensor protein Uhp
25	40	47.1	836	2	T42323	hypothetical prote
26	40	47.1	1179	2	T35093	DNA-directed DNA p
27	39	45.9	88	2	AF1023	hypothetical prote
28	39	45.9	111	2	B25159	13K sin operon hyp
29	39	45.9	279	2	D82243	transcription regu
30	39	45.9	379	2	T50967	probable pyruvate
31	39	45.9	425	2	S68305	gag polyprotein -
32	39	45.9	437	2	JC7138	alpha-amylase (EC
33	39	45.9	440	2	S14958	alpha-amylase (EC
34	39	45.9	446	2	H90063	hypothetical prote
35	39	45.9	494	2	T28660	probable adhesin P
36	39	45.9	568	2	T28876	hypothetical prote
37	39	45.9	1085	2	S55352	IFH1 protein - yea
38	39	45.9	1150	2	T15277	hypothetical prote
39	38	44.7	69	2	PC1257	alpha-amylase (EC
40	38	44.7	260	2	T22990	hypothetical prote
41	38	44.7	261	2	D86729	hypothetical prote
42	38	44.7	296	2	T12770	probable endonucle
43	38	44.7	347	2	T23944	hypothetical prote
44	38	44.7	393	2	S39383	cyclin CCL1 - yeas
45	38	44.7	415	2	B84544	probable WD-40 rep
46	38	44.7	424	2	JC7558	chromatin assembly
47	38	44.7	424	2	S17571	carboxypeptidase T
48	38	44.7	437	2	JT0946	alpha-amylase 3E -
49	38	44.7	439	2	T41966	hypothetical prote
50	38	44.7	450	2	C87463	hypothetical prote
51	38	44.7	473	2	F82561	hemolysin secretio
52	38	44.7	555	2	E87576	choline dehydrogen
53	38	44.7	742	2	H87441	hypothetical prote
54	38	44.7	768	2	S43567	R01H10.7 protein (
55	38	44.7	769	2	S35458	SNF2 protein homol
56	38	44.7	797	2	AH1302	primosomal replica
57	38	44.7	797	2	AH1674	primosomal replica
58	38	44.7	807	2	A38152	F-spondin - rat
59	38	44.7	812	2	F88577	protein R01H10.7 [
60	38	44.7	843	2	T16906	hypothetical prote
61	38	44.7	976	2	S35457	SNF2 protein homol
62	38	44.7	1403	2	S64142	hypothetical prote
63	38	44.7	2124	2	A28452	proteoglycan core
64	38	44.7	2132	1	A55182	aggrecan precursor
65	38	44.7	2257	2	D86483	protein F5J5.19 [i
66	38	44.7	2359	2	E86483	probable acetyl-Co
67	38	44.7	2748	2	S57976	nuclear migration
68	37.5	44.1	423	2	A41204	carboxypeptidase B
69	37.5	44.1	493	2	G90604	hypothetical prote

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2\_copy\_77\_91.rup.

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This page gives you Search Results detail for the Application 10616279 and Search Result us-10-616-279-2\_copy\_77\_91.rup.

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:28:34 ; Search time 153.913 Seconds  
(without alignments)  
90.150 Million cell updates/sec

Title: US-10-616-279-2\_COPY\_77\_91  
Perfect score: 85  
Sequence: 1 HSSDYSMWRKNQYVS 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	85	100.0	331	1	SPON2_HUMAN	Q9bud6 homo sapien
2	85	100.0	331	2	Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	85	100.0	331	2	Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	82	96.5	289	2	Q6KAS6_MOUSE	Q6kas6 mus musculu



5	82	96.5	330	1	SPON2_MOUSE	Q8bms2	mus musculu
6	82	96.5	330	1	SPON2_RAT	Q9wv75	rattus norv
7	82	96.5	330	2	Q8VD28_MOUSE	Q8vd28	mus musculu
8	63	74.1	331	2	O42112_BRARE	O42112	brachydanio
9	57	67.1	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon n
10	55	64.7	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus lae
11	49	57.6	138	2	Q82UD3_NITEU	Q82ud3	nitrosomona
12	49	57.6	420	2	O22019_CYAME	O22019	cyanidiosch
13	49	57.6	446	2	Q85G84_CYAME	Q85g84	cyanidiosch
14	49	57.6	919	2	Q2XVY3_PUCGR	Q2xvy3	puccinia gr
15	47	55.3	103	2	Q3YJU0_BIOGL	Q3yju0	biomphalari
16	47	55.3	390	2	Q7Y4U7_BPR69	Q7y4u7	bacterioph
17	47	55.3	924	2	Q56B07_TREHY	Q56b07	treponema h
18	46	54.1	438	1	AMY1_HORVU	P00693	hordeum vul
19	46	54.1	438	2	Q40017_HORVU	Q40017	hordeum vul
20	46	54.1	1453	2	Q755D1_ASHGO	Q755d1	ashbya goss
21	45	52.9	430	2	Q58TI0_9GOBI	Q58ti0	elacatinus
22	45	52.9	430	2	Q58TI1_9GOBI	Q58ti1	elacatinus
23	45	52.9	430	2	Q58TI2_9GOBI	Q58ti2	elacatinus
24	45	52.9	430	2	Q58TI3_9GOBI	Q58ti3	elacatinus
25	45	52.9	724	2	Q57QF1_SALCH	Q57qf1	salmonella
26	45	52.9	845	2	Q4QG81_LEIMA	Q4qg81	leishmania
27	44.5	52.4	1091	2	Q54M12_DICDI	Q54ml2	dictyosteli
28	44	51.8	251	2	Q5FVN7_RAT	Q5fvn7	rattus norv
29	44	51.8	314	2	Q4NCJ0_9MICC	Q4ncj0	arthrobacte
30	44	51.8	376	2	Q57YS2_9TRYP	Q57ys2	trypanosoma
31	44	51.8	396	2	Q4CPW5_TRYCR	Q4cpw5	trypanosoma
32	44	51.8	396	2	Q57YS1_9TRYP	Q57ys1	trypanosoma
33	44	51.8	429	2	Q3R0P7_XYLFA	Q3r0p7	xylella fas
34	44	51.8	429	2	Q3RGQ3_XYLFA	Q3rgq3	xylella fas
35	44	51.8	434	2	O81699_AVEFA	O81699	avena fatua
36	44	51.8	434	2	Q87CW9_XYLFT	Q87cw9	xylella fas
37	44	51.8	437	2	O81700_AVEFA	O81700	avena fatua
38	44	51.8	839	2	Q8ML26_DROME	Q8ml26	drosophila
39	44	51.8	2889	2	Q38CF1_9TRYP	Q38cf1	trypanosoma
40	44	51.8	3099	2	Q7R5I4_GIALA	Q7r5i4	giardia lam
41	43.5	51.2	545	1	MED17_SCHPO	P87306	schizosacch
42	43.5	51.2	570	2	Q8D4R4_VIBVU	Q8d4r4	vibrio vuln
43	43.5	51.2	602	2	Q7MGB8_VIBVY	Q7mgb8	vibrio vuln
44	43	50.6	86	2	Q3J7I8_NITOC	Q3j7i8	nitrosococc
45	43	50.6	163	2	Q3SS72_NITWN	Q3ss72	nitrobacter
46	43	50.6	173	2	Q302Z8_STRSU	Q302z8	streptococc
47	43	50.6	185	2	Q3PNI1_NITHA	Q3pni1	nitrobacter
48	43	50.6	273	1	HIS6_METAC	Q8tt96	methanosarc
49	43	50.6	322	2	Q59WG7_CANAL	Q59wg7	candida alb
50	43	50.6	463	2	Q89KW8_BRAJA	Q89kw8	bradyrhizob
51	43	50.6	809	2	Q7NAF2_MYCGA	Q7naf2	mycoplasma
52	43	50.6	1383	2	Q3KF64_PSEPF	Q3kf64	pseudomonas
53	42	49.4	92	2	Q6DC15_BRARE	Q6dc15	brachydanio
54	42	49.4	105	2	Q739L5_BACC1	Q739l5	bacillus ce
55	42	49.4	206	2	Q99L35_MOUSE	Q99l35	mus musculu
56	42	49.4	230	2	Q7T5M1_GVCL	Q7t5m1	cryptophleb
57	42	49.4	239	2	Q8JRZ0_9BACU	Q8jrz0	phthorimaea
58	42	49.4	245	2	Q4HIG6_CAMCO	Q4hig6	campylobact
59	42	49.4	294	1	TSN15_HUMAN	O95858	homo sapien
60	42	49.4	331	2	Q3TA07_MOUSE	Q3ta07	mus musculu
61	42	49.4	411	2	Q5A3N9_CANAL	Q5a3n9	candida alb
62	42	49.4	411	2	Q5A3V3_CANAL	Q5a3v3	candida alb
63	42	49.4	422	2	Q6YQR6_ONYPE	Q6yqr6	onion yello
64	42	49.4	436	1	AM3D_ORYSA	P27933	oryza sativ
65	42	49.4	441	2	Q2ST11_MYCCA	Q2st11	mycoplasma

**SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.rag.**

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OM protein - protein search, using sw model

```
Run on:      May 25, 2006, 11:55:15 ; Search time 271.158 Seconds
              (without alignments)
              558.119 Million cell updates/sec
```

```
Title:          US-10-616-279-2
Perfect score: 1760
Sequence:      1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECPDNCV 331
```

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1760	100.0	331	4	AAB82472	Aab82472 Human ext
2	1760	100.0	331	9	ADW76921	Adw76921 Human RG1
3	1752	99.5	331	4	AAM93324	Aam93324 Human pol
4	1752	99.5	331	5	ABG61806	Abg61806 Prostate
5	1752	99.5	331	5	AAU79944	Aau79944 Human Spo
6	1752	99.5	331	5	ABB77393	Abb77393 Human spo
7	1752	99.5	331	7	ADB75561	Adb75561 Prostate
8	1752	99.5	331	7	ADG42585	Adg42585 Human ext
9	1752	99.5	331	7	ADN38814	Adn38814 Cancer/an
10	1752	99.5	331	7	ADN39877	Adn39877 Cancer/an
11	1752	99.5	331	8	ADJ75655	Adj75655 Marker ge
12	1752	99.5	331	8	ADL30814	Adl30814 Human pro
13	1752	99.5	331	8	ADO20071	Ado20071 Human PRO
14	1752	99.5	331	8	ADQ18813	Adq18813 Human sof
15	1752	99.5	331	8	ADT50838	Adt50838 Cancer re
16	1752	99.5	331	8	ADU06656	Adu06656 Novel bro
17	1752	99.5	422	8	ADR66362	Adr66362 Human pro
18	1752	99.5	422	8	ADR66704	Adr66704 Human pro
19	1749	99.4	331	4	AAM38872	Aam38872 Human pol
20	1749	99.4	444	4	AAM40658	Aam40658 Human pol
21	1747	99.3	331	3	AAV79561	Aay79561 Cancer sp
22	1747	99.3	349	9	AEA05999	Aea05999 His-tagge
23	1744	99.1	331	2	AAW70589	Aaw70589 Adhesion-
24	1744	99.1	331	2	AAV41721	Aay41721 Human PRO
25	1744	99.1	331	3	AAB33465	Aab33465 Human PRO
26	1744	99.1	331	3	AAB44277	Aab44277 Human PRO
27	1744	99.1	331	3	AAV95349	Aay95349 Human PRO
28	1744	99.1	331	4	AAM93266	Aam93266 Human pol
29	1744	99.1	331	5	AAE20463	Aae20463 Human tum
30	1744	99.1	331	6	ABO25223	Abo25223 Novel hum
31	1744	99.1	331	6	ABU72229	Abu72229 Novel hum
32	1744	99.1	331	6	ABU84909	Abu84909 Human sec
33	1744	99.1	331	6	ABU61107	Abu61107 Human PRO
34	1744	99.1	331	6	ABU80376	Abu80376 Human sec
35	1744	99.1	331	6	ABG75949	Abg75949 Human ant
36	1744	99.1	331	6	ADA24775	Ada24775 Novel hum
37	1744	99.1	331	6	ABO19678	Abo19678 Novel hum
38	1744	99.1	331	6	ADA12436	Ada12436 Human sec
39	1744	99.1	331	6	ABO19569	Abo19569 Novel hum
40	1744	99.1	331	7	ADB73742	Adb73742 Human PRO
41	1744	99.1	331	7	ADB76458	Adb76458 Human PRO
42	1744	99.1	331	7	ADC43884	Adc43884 Human sec
43	1744	99.1	331	7	ADC61644	Adc61644 Human sec
44	1744	99.1	331	7	ADC63608	Adc63608 Human sec
45	1744	99.1	331	7	ADC66708	Adc66708 Human sec

## ALIGNMENTS

## RESULT 1

AAB82472

ID AAB82472 standard; protein; 331 AA.

XX

AC AAB82472;

XX

DT 22-AUG-2001 (first entry)

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra1.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:07:05 ; Search time 69.1921 Seconds  
(without alignments)  
418.728 Million cell updates/sec

Title: US-10-616-279-2  
Perfect score: 1760  
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECVPDNCV 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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1	1760	100.0	331	2	US-09-732-357B-2	Sequence 2, Appli
2	1752	99.5	331	2	US-09-949-002-397	Sequence 397, App
3	1747	99.3	331	2	US-09-807-200-2	Sequence 2, Appli
4	1744	99.1	331	2	US-09-999-833A-236	Sequence 236, App
5	1744	99.1	331	2	US-10-020-445A-236	Sequence 236, App
6	1744	99.1	331	2	US-09-978-189-236	Sequence 236, App
7	1744	99.1	331	2	US-10-017-085A-236	Sequence 236, App
8	1744	99.1	331	3	US-10-145-129A-236	Sequence 236, App
9	1744	99.1	331	3	US-10-013-929A-236	Sequence 236, App
10	1744	99.1	331	3	US-10-013-917A-236	Sequence 236, App
11	1744	99.1	422	2	US-09-949-002-504	Sequence 504, App
12	1742	99.0	331	1	US-08-799-173A-2	Sequence 2, Appli
13	1742	99.0	331	2	US-09-170-042A-2	Sequence 2, Appli
14	1551.5	88.2	330	2	US-09-371-696-2	Sequence 2, Appli
15	1506.5	85.6	330	2	US-09-732-357B-13	Sequence 13, Appl
16	1101.5	62.6	299	2	US-09-311-021-202	Sequence 202, App
17	464.5	26.4	802	1	US-07-862-021B-12	Sequence 12, Appl
18	464.5	26.4	802	1	US-08-313-288B-12	Sequence 12, Appl
19	464.5	26.4	802	5	PCT-US93-03164-12	Sequence 12, Appl
20	462.5	26.3	392	1	US-08-799-173A-7	Sequence 7, Appli
21	462.5	26.3	392	2	US-09-170-042A-7	Sequence 7, Appli
22	462.5	26.3	807	1	US-07-862-021B-10	Sequence 10, Appl
23	462.5	26.3	807	1	US-08-313-288B-10	Sequence 10, Appl
24	462.5	26.3	807	2	US-09-132-769-5	Sequence 5, Appli
25	462.5	26.3	807	5	PCT-US93-03164-10	Sequence 10, Appl
26	460.5	26.2	787	2	US-09-825-294-207	Sequence 207, App
27	460.5	26.2	787	2	US-09-970-966-207	Sequence 207, App
28	460.5	26.2	807	2	US-09-132-769-1	Sequence 1, Appli
29	460.5	26.2	807	2	US-09-132-769-3	Sequence 3, Appli
30	460.5	26.2	807	2	US-09-640-173-186	Sequence 186, App
31	460.5	26.2	807	2	US-09-713-550-186	Sequence 186, App
32	460.5	26.2	807	2	US-09-825-294-186	Sequence 186, App
33	460.5	26.2	807	2	US-09-970-966-186	Sequence 186, App
34	438.5	24.9	819	2	US-09-270-767-42963	Sequence 42963, A
35	422.5	24.0	677	2	US-09-270-767-58094	Sequence 58094, A
36	422.5	24.0	847	2	US-09-270-767-42783	Sequence 42783, A
37	420.5	23.9	132	2	US-09-022-238-2	Sequence 2, Appli
38	331	18.8	568	1	US-07-862-021B-14	Sequence 14, Appl
39	331	18.8	568	5	PCT-US93-03164-14	Sequence 14, Appl
40	309	17.6	53	1	US-08-799-173A-18	Sequence 18, Appl
41	309	17.6	53	2	US-09-170-042A-19	Sequence 19, Appl
42	189	10.7	37	2	US-09-022-238-3	Sequence 3, Appli
43	181	10.3	37	2	US-09-371-696-3	Sequence 3, Appli
44	134	7.6	1588	3	US-10-000-512-2	Sequence 2, Appli
45	130.5	7.4	56	1	US-07-862-021B-19	Sequence 19, Appl

## ALIGNMENTS

## RESULT 1

US-09-732-357B-2

; Sequence 2, Application US/09732357B

; Patent No. 6682902

## ; GENERAL INFORMATION:

; APPLICANT: Harkins, Richard

; APPLICANT: Parkes, Deborah

; APPLICANT: Parry, Gordon

; APPLICANT: Schneider, Douglas

; APPLICANT: Steinbrecher, Renate

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:39 ; Search time 230.952 Seconds  
(without alignments)  
663.879 Million cell updates/sec

Title: US-10-616-279-2  
Perfect score: 1760  
Sequence: 1 MENPSPAAALGKALCALLA.....NGSPCPELEEEAECPDNCV 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1760	100.0	331	3	US-09-732-357A-2	Sequence 2, Appli
2	1760	100.0	331	4	US-10-616-279-2	Sequence 2, Appli
3	1760	100.0	331	4	US-10-624-884-2	Sequence 2, Appli

4	1760	100.0	331	5	US-10-895-183-2	Sequence 2, Appli
5	1752	99.5	331	3	US-09-970-944-12	Sequence 12, Appl
6	1752	99.5	331	3	US-09-970-944-38	Sequence 38, Appl
7	1752	99.5	331	4	US-10-205-823-385	Sequence 385, App
8	1752	99.5	331	4	US-10-295-027-132	Sequence 132, App
9	1752	99.5	331	4	US-10-295-027-1195	Sequence 1195, Ap
10	1752	99.5	331	5	US-10-723-860-1632	Sequence 1632, Ap
11	1752	99.5	331	5	US-10-631-467-907	Sequence 907, App
12	1752	99.5	331	6	US-11-051-454-385	Sequence 385, App
13	1752	99.5	331	6	US-11-203-526-40	Sequence 40, Appl
14	1747	99.3	331	5	US-10-929-973-2	Sequence 2, Appli
15	1747	99.3	349	5	US-10-919-215-1	Sequence 1, Appli
16	1744	99.1	331	3	US-09-978-295A-236	Sequence 236, App
17	1744	99.1	331	3	US-09-938-418-8	Sequence 8, Appli
18	1744	99.1	331	3	US-09-978-697-236	Sequence 236, App
19	1744	99.1	331	3	US-09-978-192A-236	Sequence 236, App
20	1744	99.1	331	3	US-09-999-832A-236	Sequence 236, App
21	1744	99.1	331	3	US-09-978-189-236	Sequence 236, App
22	1744	99.1	331	3	US-09-978-608A-236	Sequence 236, App
23	1744	99.1	331	3	US-09-978-585A-236	Sequence 236, App
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27	1744	99.1	331	3	US-09-999-833A-236	Sequence 236, App
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29	1744	99.1	331	3	US-09-978-824-236	Sequence 236, App
30	1744	99.1	331	3	US-09-918-585A-236	Sequence 236, App
31	1744	99.1	331	3	US-09-999-834A-236	Sequence 236, App
32	1744	99.1	331	3	US-09-978-423A-236	Sequence 236, App
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37	1744	99.1	331	3	US-09-978-643A-236	Sequence 236, App
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41	1744	99.1	331	3	US-09-978-681A-236	Sequence 236, App
42	1744	99.1	331	3	US-09-978-194A-236	Sequence 236, App
43	1744	99.1	331	3	US-09-999-829A-236	Sequence 236, App
44	1744	99.1	331	3	US-09-978-299A-236	Sequence 236, App
45	1744	99.1	331	3	US-09-978-544A-236	Sequence 236, App

## ALIGNMENTS

## RESULT 1

US-09-732-357A-2

; Sequence 2, Application US/09732357A

; Patent No. US20020004047A1

; GENERAL INFORMATION:

; APPLICANT: Harkins, Richard

; APPLICANT: Parkes, Deborah

; APPLICANT: Parry, Gordon

; APPLICANT: Schneider, Douglas

; APPLICANT: Steinbrecher, Renate

; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1e1 RG-1 Polypeptide

; FILE REFERENCE: 51791AUSM1

; CURRENT APPLICATION NUMBER: US/09/732,357A

; CURRENT FILING DATE: 2001-05-14

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.ra

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:23:59 ; Search time 14.9605 Seconds  
(without alignments)  
246.414 Million cell updates/sec

Title: US-10-616-279-2  
Perfect score: 1760  
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECPDNCV 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	107	6.1	236	7 US-11-293-697-4829	Sequence 4829, Ap



2	98.5	5.6	5738	6	US-10-505-928-150	Sequence 150, App
3	98	5.6	1126	7	US-11-293-697-3665	Sequence 3665, Ap
4	83.5	4.7	548	6	US-10-548-484-78	Sequence 78, Appl
5	83	4.7	778	7	US-11-293-697-3043	Sequence 3043, Ap
6	81	4.6	406	6	US-10-953-349-31643	Sequence 31643, A
7	80.5	4.6	343	6	US-10-953-349-26233	Sequence 26233, A
8	80.5	4.6	743	7	US-11-293-697-4198	Sequence 4198, Ap
9	80	4.5	341	6	US-10-196-749-224	Sequence 224, App
10	79.5	4.5	258	6	US-10-196-749-284	Sequence 284, App
11	79.5	4.5	612	6	US-10-953-349-19032	Sequence 19032, A
12	79.5	4.5	631	6	US-10-953-349-19031	Sequence 19031, A
13	79.5	4.5	661	6	US-10-953-349-19030	Sequence 19030, A
14	79	4.5	429	6	US-10-953-349-32400	Sequence 32400, A
15	79	4.5	786	6	US-10-953-349-9018	Sequence 9018, Ap
16	78.5	4.5	694	6	US-10-505-928-312	Sequence 312, App
17	78	4.4	406	7	US-11-185-204A-2	Sequence 2, Appli
18	78	4.4	406	7	US-11-185-215A-2	Sequence 2, Appli
19	78	4.4	496	7	US-11-293-697-2541	Sequence 2541, Ap
20	78	4.4	582	7	US-11-293-697-3683	Sequence 3683, Ap
21	77.5	4.4	213	6	US-10-953-349-28731	Sequence 28731, A
22	77.5	4.4	213	6	US-10-953-349-33732	Sequence 33732, A
23	77.5	4.4	243	6	US-10-953-349-28730	Sequence 28730, A
24	77	4.4	612	6	US-10-953-349-11169	Sequence 11169, A
25	77	4.4	620	7	US-11-293-697-3458	Sequence 3458, Ap
26	77	4.4	634	6	US-10-953-349-11168	Sequence 11168, A
27	77	4.4	650	6	US-10-953-349-11167	Sequence 11167, A
28	76.5	4.3	369	7	US-11-293-697-3622	Sequence 3622, Ap
29	76.5	4.3	473	6	US-10-953-349-10337	Sequence 10337, A
30	76.5	4.3	491	6	US-10-953-349-10336	Sequence 10336, A
31	76.5	4.3	506	6	US-10-953-349-10335	Sequence 10335, A
32	76	4.3	238	6	US-10-953-349-11456	Sequence 11456, A
33	76	4.3	613	7	US-11-293-697-4125	Sequence 4125, Ap
34	76	4.3	639	7	US-11-246-999-33	Sequence 33, Appl
35	76	4.3	1456	6	US-10-505-928-69	Sequence 69, Appl
36	75.5	4.3	173	6	US-10-953-349-23419	Sequence 23419, A
37	75.5	4.3	293	6	US-10-953-349-31470	Sequence 31470, A
38	75.5	4.3	410	6	US-10-953-349-36013	Sequence 36013, A
39	75.5	4.3	448	6	US-10-953-349-36012	Sequence 36012, A
40	75	4.3	149	6	US-10-953-349-25513	Sequence 25513, A
41	75	4.3	171	6	US-10-953-349-21189	Sequence 21189, A
42	75	4.3	180	6	US-10-953-349-21188	Sequence 21188, A
43	75	4.3	187	6	US-10-953-349-21187	Sequence 21187, A
44	75	4.3	210	6	US-10-953-349-21439	Sequence 21439, A
45	75	4.3	260	6	US-10-953-349-25808	Sequence 25808, A

## ALIGNMENTS

## RESULT 1

US-11-293-697-4829

; Sequence 4829, Application US/11293697

; Publication No. US20060105376A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: H1-A0106

; CURRENT APPLICATION NUMBER: US/11/293,697

; CURRENT FILING DATE: 2005-12-05

; PRIOR APPLICATION NUMBER: US/10/108,260

; PRIOR FILING DATE: 2002-03-28

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OM protein - protein search, using sw model

Run on: May 25, 2006, 12:00:39 ; Search time 44.8814 Seconds  
(without alignments)  
709.599 Million cell updates/sec

Title: US-10-616-279-2  
Perfect score: 1760  
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECVPDNCV 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	462.5	26.3	807	2	A38152	F-spondin - rat
2	448.5	25.5	803	2	A47723	F-spondin precursor
3	401	22.8	805	2	T34212	hypothetical prote
4	122.5	7.0	741	2	I48694	probable transcrip
5	117.5	6.7	770	2	D89447	protein F57C12.1 [
6	112	6.4	772	2	A55004	transcription fact
7	108	6.1	123	2	S49108	TRAP-C2 protein -
8	107	6.1	808	2	T10171	phospholipase D (E

9	104.5	5.9	440	2	T24232	hypothetical prote
10	103	5.9	742	2	A49672	transcription fact
11	102	5.8	1251	2	A57293	latent transformin
12	100.5	5.7	810	2	D96566	hypothetical prote
13	100.5	5.7	2957	2	T33152	hypothetical prote
14	99.5	5.7	590	2	I46687	complement compone
15	99.5	5.7	724	2	A48569	antigen Em100 - Ei
16	99.5	5.7	812	2	T03659	phospholipase D (E
17	98	5.6	903	2	T00705	N-chimerin homolog
18	97.5	5.5	808	2	T04092	phospholipase D (E
19	97	5.5	534	2	T41081	hypothetical prote
20	97	5.5	1360	2	T33922	hypothetical prote
21	96.5	5.5	598	2	A57249	beta-galactosidase
22	96.5	5.5	712	2	A45638	immunodominant mic
23	96.5	5.5	812	2	T03402	probable phospholi
24	96.5	5.5	912	2	A54423	brevican precursor
25	96.5	5.5	1572	2	T00027	brain-specific ang
26	96	5.5	591	1	C8HUB	complement C8 beta
27	96	5.5	1584	2	T00026	brain-specific ang
28	94	5.3	809	2	T11695	phospholipase D (E
29	93	5.3	483	1	VCBPI3	minor coat protein
30	92	5.2	1306	2	S25370	MSB2 protein - yea
31	91.5	5.2	424	2	C70651	hypothetical prote
32	91	5.2	152	2	D89753	protein F11C7.2 [i
33	91	5.2	862	2	T46289	hypothetical prote
34	91	5.2	937	2	D87483	ribonucleotide red
35	90	5.1	497	2	T41015	proline rich prote
36	90	5.1	692	2	AD1857	hypothetical prote
37	90	5.1	1444	2	T18856	angiogenesis inhib
38	90	5.1	1666	2	T43169	hypothetical prote
39	90	5.1	2265	1	FNBO	fibronectin - bovi
40	90	5.1	3027	2	JQ1917	polyprotein - pars
41	89.5	5.1	919	2	T32541	unc-5 protein - Ca
42	89.5	5.1	947	1	B44294	unc-5 protein, lon
43	89	5.1	649	2	D96025	probable adenylate
44	89	5.1	697	2	T03834	nuclear distributi
45	89	5.1	1257	2	T09493	period protein hom

## ALIGNMENTS

## RESULT 1

A38152

F-spondin - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A38152

R;Klar, A.; Baldassare, M.; Jessell, T.M.

Cell 69, 95-110, 1992

A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secre

A;Reference number: A38152; MUID:92208952; PMID:1555244

A;Accession: A38152

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-807

A;Cross-references: UNIPROT:P35446; UNIPARC:UPI000012AC71; GB:M88469; NID:g204176; PID

A;Experimental source: embryo floor plate

A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)

C;Superfamily: F-spondin; thrombospondin type 1 repeat homology

F;441-495/Domain: thrombospondin type 1 repeat homology

# SCORE Search Results Details for Application 10616279 and Search Result us-10-616-279-2.rup.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:55:28 ; Search time 359.051 Seconds  
(without alignments)  
852.749 Million cell updates/sec

Title: US-10-616-279-2  
Perfect score: 1760  
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCPELEEEAECPDNCV 331

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1744	99.1	331	1 SPON2_HUMAN	Q9bud6 homo sapien
2	1742	99.0	331	2 Q4W5N4_HUMAN	Q4w5n4 homo sapien
3	1716	97.5	331	2 Q5RFG6_PONPY	Q5rfg6 pongo pygma
4	1506.5	85.6	330	1 SPON2_RAT	Q9wv75 rattus norv

5	1494.5	84.9	330	1	SPON2_MOUSE	Q8bms2	mus	musculu
6	1488.5	84.6	330	2	Q8VD28_MOUSE	Q8vd28	mus	musculu
7	1403	79.7	289	2	Q6KAS6_MOUSE	Q6kas6	mus	musculu
8	1113.5	63.3	313	2	Q6DCM4_XENLA	Q6dcm4	xenopus	lae
9	1108	63.0	331	2	O42112_BRARE	O42112	brachydanio	
10	1073.5	61.0	355	2	Q4SQV5_TETNG	Q4sqv5	tetraodon	n
11	871	49.5	334	2	O42111_BRARE	O42111	brachydanio	
12	733	41.6	280	2	Q4SDS0_TETNG	Q4sds0	tetraodon	n
13	568	32.3	129	2	Q3TEM5_MOUSE	Q3tem5	mus	musculu
14	522.5	29.7	601	2	Q9V746_DROME	Q9v746	drosophila	
15	512	29.1	598	2	O02029_DROME	O02029	drosophila	
16	483.5	27.5	557	2	Q4SPB7_TETNG	Q4spb7	tetraodon	n
17	470.5	26.7	808	2	O42113_BRARE	O42113	brachydanio	
18	468.5	26.6	806	2	Q4SOW9_TETNG	Q4sow9	tetraodon	n
19	466	26.5	729	2	Q69ZZ7_MOUSE	Q69zz7	mus	musculu
20	464.5	26.4	802	1	SPON1_CHICK	Q9w770	gallus	gall
21	462.5	26.3	807	1	SPON1_MOUSE	Q8vcc9	mus	musculu
22	462.5	26.3	807	1	SPON1_RAT	P35446	rattus	norv
23	462.5	26.3	807	2	Q3B7D6_RAT	Q3b7d6	rattus	norv
24	460.5	26.2	807	1	SPON1_BOVIN	Q9glx9	bos	taurus
25	460.5	26.2	807	1	SPON1_HUMAN	Q9hcb6	homo	sapien
26	457	26.0	898	2	O76822_BRAFL	O76822	branchiosto	
27	448.5	25.5	803	1	SPON1_XENLA	P35447	xenopus	lae
28	447	25.4	628	2	Q7KRF4_DROME	Q7krf4	drosophila	
29	447	25.4	763	2	Q9XZD0_DROME	Q9xzd0	drosophila	
30	443	25.2	803	2	O42114_BRARE	O42114	brachydanio	
31	441.5	25.1	873	2	Q7KR42_DROME	Q7kr42	drosophila	
32	440.5	25.0	505	2	Q5TN62_ANOGA	Q5tn62	anopheles	g
33	440.5	25.0	845	2	Q7Q082_ANOGA	Q7q082	anopheles	g
34	439.5	25.0	781	2	Q7PZ75_ANOGA	Q7pz75	anopheles	g
35	436	24.8	632	2	Q5TMM3_ANOGA	Q5tmm3	anopheles	g
36	424.5	24.1	839	2	Q8ML26_DROME	Q8ml26	drosophila	
37	420.5	23.9	216	2	Q9H7I1_HUMAN	Q9h7i1	homo	sapien
38	401	22.8	819	2	Q19305_CAEEL	Q19305	caenorhabdi	
39	400	22.7	820	2	Q61C53_CAEER	Q61c53	caenorhabdi	
40	374	21.2	924	2	Q3ZAL6_DROME	Q3zal6	drosophila	
41	306	17.4	861	2	Q8ML27_DROME	Q8ml27	drosophila	
42	280.5	15.9	549	2	Q8T988_DROME	Q8t988	drosophila	
43	271.5	15.4	461	2	Q95S22_DROME	Q95s22	drosophila	
44	225.5	12.8	92	2	Q6DC15_BRARE	Q6dc15	brachydanio	
45	167.5	9.5	78	2	Q4SDS1_TETNG	Q4sds1	tetraodon	n

## ALIGNMENTS

## RESULT 1

## SPON2\_HUMAN

ID SPON2\_HUMAN STANDARD; PRT; 331 AA.

AC Q9BUD6; Q9ULW1;

DT 27-SEP-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 30.

DE Spondin-2 precursor (Mindin) (Differentially expressed in cancerous and noncancerous lung cells 1) (DIL-1).

GN Name=SPON2; Synonyms=DIL1; ORFNames=UNQ435/PRO866;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;